

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 09:44:34 ; Search time 39 Seconds  
(without alignments)  
420.014 Million cell updates/sec

Title: US-09-703-350B-76

Perfect score: 1268

Sequence: 1 MLQNSAVLLVVISASATHE.....NLRGEDSPSHIKRTSHSA 247

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

- Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1268	100.0	247	2	US-08-208-005C-2
2	1268	100.0	247	2	US-09-038-597A-2
3	1268	100.0	247	2	US-08-460-529B-10
4	1268	100.0	247	2	US-08-431-117A-2
5	1268	100.0	247	2	US-09-361-736B-10
6	660.5	52.1	204	2	US-08-208-005C-5
7	660.5	52.1	204	2	US-09-038-597A-5
8	628	49.5	170	4	US-08-460-529B-9
9	628	49.5	170	4	US-09-361-736B-9
10	354.5	28.0	296	3	US-08-831-132-14
11	354.5	28.0	296	3	US-09-416-150-14
12	354	27.9	302	3	US-08-831-132-2
13	354	27.9	302	3	US-09-416-150-2
14	354	27.9	302	3	US-09-193-881-23
15	354	27.9	302	4	US-09-361-736B-12
16	351.5	27.7	251	4	US-09-361-736B-2
17	333.5	26.3	251	2	US-08-460-529B-2
18	91	7.2	901	4	US-09-828-062-8
19	89.5	7.1	10182	3	US-09-134-001C-3159
20	86	6.8	500	4	US-09-198-452A-299
21	85.5	6.7	311	4	US-09-710-279-2460
22	85.5	6.7	656	3	US-09-134-001C-4322
23	83.5	6.6	290	4	US-09-655-908-6
24	83.5	6.6	290	4	US-09-655-908-8
25	83.5	6.6	1027	4	US-09-762-724-8
26	83.5	6.6	1027	4	US-09-762-724-6
27	83	6.5	319	4	US-09-710-279-792

28	83	6.5	319	4	US-09-710-279-2008	Sequence 2008, Ap
29	83	6.5	398	4	US-09-710-279-444	Sequence 44, Appl
30	83	6.5	398	4	US-09-710-279-1498	Sequence 1498, Ap
31	83	6.5	417	3	US-09-134-001C-3810	Sequence 3810, Ap
32	82	6.5	362	3	US-09-134-001C-4670	Sequence 4670, Ap
33	81	6.4	680	3	US-09-298-924-4	Sequence 4, Appl1
34	81	6.4	720	2	US-08-840-236-1	Sequence 1, Appl1
35	81	6.4	720	2	US-08-505-448A-1	Sequence 1, Appl1
36	79.5	6.3	609	4	US-09-538-092-711	Sequence 711, App
37	79.5	6.3	708	1	US-08-145-681-4	Sequence 4, Appl1
38	79.5	6.3	708	1	US-08-453-703-4	Sequence 4, Appl1
39	79.5	6.3	708	2	US-08-456-106-4	Sequence 4, Appl1
40	79.5	6.3	708	3	US-08-456-108-4	Sequence 4, Appl1
41	79.5	6.3	708	3	US-09-265-577-4	Sequence 4, Appl1
42	79.5	6.3	708	4	US-09-633-739-4	Sequence 4, Appl1
43	79.5	6.2	264	4	US-09-134-000C-5831	Sequence 5831, Ap
44	78.5	6.2	1288	4	US-09-546-934-4	Sequence 4, Appl1
45	78	6.2	315	3	US-09-184-964-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1  
US-08-208-005C-2  
; Sequence 2, Application US/08208005C  
; Patent No. 5837498  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Capsules of Stannius Protein, Stannicalcin  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GIUFFRAN,  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/208,005C  
; FILING DATE: 8 MARCH 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-78  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 247 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
; US-08-208-005C-2  
Query Match 100.0%; Score 1268; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1,6e-136;  
Matches 247; Conservative 0; Mismatches 0; Gaps 0;  
1 MLQNSAVLLVVISASATHEAQNDSVSPKRSVAQNSAEVYRCINSLAQVGGAGAC 60  
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Db 1 MLNSAVLLVIVISASATHEAEONDSVSPRKSRAVAQAQNSAEVVRCLNSALQVCGCAFACL 60  
QY 61 ENSTCTDGMWDICSFYSAKAFDTQGAFFYKESLKCICANGVTSKVFIAIRRCSTFFORM 120  
Db 61 ENSTCTDGMWDICSFYSAKAFDTQGAFFYKESLKCICANGVTSKVFIAIRRCSTFFORM 120  
QY 121 IAEVQECYCKLVNCSIAKRNPEALTEVQOLPHFNSRYYNRLVRSLLCEDEDTVSTIRD 180  
Db 121 IAEVQECYCKLVNCSIAKRNPEALTEVQOLPHFNSRYYNRLVRSLLCEDEDTVSTIRD 180  
QY 181 SLMEKIGPMNASLFIHLQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGDEDSPSHIK 240  
Db 181 SLMEKIGPMNASLFIHLQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGDEDSPSHIK 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 2  
US-09-038-597A-2  
Sequence 2, Application US/09038597A  
Patent No. 5877290  
GENERAL INFORMATION:  
APPLICANT: OLSEN, ET AL.  
TITLE OF INVENTION: Copuscles of Stannius Protein,  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,597A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/208,005  
FILING DATE: 8-MARCH-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-78  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-09-038-597A-2

Query Match 100.0%; Score 1268; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1.6e-136;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLNSAVLLVIVISASATHEAEONDSVSPRKSRAVAQAQNSAEVVRCLNSALQVCGCAFACL 60  
Db 1 MLNSAVLLVIVISASATHEAEONDSVSPRKSRAVAQAQNSAEVVRCLNSALQVCGCAFACL 60  
QY 61 ENSTCTDGMWDICSFYSAKAFDTQGAFFYKESLKCICANGVTSKVFIAIRRCSTFFORM 120

Db 61 ENSTCTDGMWDICSFYSAKAFDTQGAFFYKESLKCICANGVTSKVFIAIRRCSTFFORM 120  
QY 121 IAEVQECYCKLVNCSIAKRNPEALTEVQOLPHFNSRYYNRLVRSLLCEDEDTVSTIRD 180  
Db 121 IAEVQECYCKLVNCSIAKRNPEALTEVQOLPHFNSRYYNRLVRSLLCEDEDTVSTIRD 180  
QY 181 SLMEKIGPMNASLFIHLQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGDEDSPSHIK 240  
Db 181 SLMEKIGPMNASLFIHLQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGDEDSPSHIK 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 3  
US-08-460-529B-10  
Sequence 10, Application US/08460529B  
Patent No. 5994103  
GENERAL INFORMATION:  
APPLICANT: OLSEN, ET AL.  
TITLE OF INVENTION: Human Stannocalcin-alpha  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,529B  
FILING DATE: June 2, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/13206  
FILING DATE: 10 NOV 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: MULLINS, J.G.  
REGISTRATION NUMBER: 33,073  
REFERENCE/DOCKET NUMBER: 325800-334 (PF143)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-08-460-529B-10

Query Match 100.0%; Score 1268; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1.6e-136;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLNSAVLLVIVISASATHEAEONDSVSPRKSRAVAQAQNSAEVVRCLNSALQVCGCAFACL 60  
Db 1 MLNSAVLLVIVISASATHEAEONDSVSPRKSRAVAQAQNSAEVVRCLNSALQVCGCAFACL 60  
QY 61 ENSTCTDGMWDICSFYSAKAFDTQGAFFYKESLKCICANGVTSKVFIAIRRCSTFFORM 120  
Db 61 ENSTCTDGMWDICSFYSAKAFDTQGAFFYKESLKCICANGVTSKVFIAIRRCSTFFORM 120  
QY 121 IAEVQECYCKLVNCSIAKRNPEALTEVQOLPHFNSRYYNRLVRSLLCEDEDTVSTIRD 180

Db 121 IAEVQECISKLVNCSIAKRNPEALTEVVOLEPHNSNRYNRLVSLLECEDETVSTIRD 180  
QY 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLGGEEDSPSHIK 240  
Db 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLGGEEDSPSHIK 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 4  
US-08-431-117A-2  
; Sequence 2, Application US/08431117A  
; Patent No. 5994301  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stannocalcin  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSER: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/431,117A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/208,005  
; FILING DATE: 8 MARCH 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-296  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 247 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
US-08-431-117A-2

Query Match 100.0%; Score 1268; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1,6e-136;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLQNSAVLVLVISASATHEAQNDSVSPKSRVAAQNSAEVVRCLNSALQVGGCAFACL 60  
Db 1 MLQNSAVLVLVISASATHEAQNDSVSPKSRVAAQNSAEVVRCLNSALQVGGCAFACL 60  
QY 61 ENSTCDTDGMYDICKSLYSAKFTDQGAFFVESLKCICANGVTSKVFLAIRRCSSTFORM 120  
Db 61 ENSTCDTDGMYDICKSLYSAKFTDQGAFFVESLKCICANGVTSKVFLAIRRCSSTFORM 120  
QY 121 IAEVQECISKLVNCSIAKRNPEALTEVVOLEPHNSNRYNRLVSLLECEDETVSTIRD 180  
Db 121 IAEVQECISKLVNCSIAKRNPEALTEVVOLEPHNSNRYNRLVSLLECEDETVSTIRD 180  
QY 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLGGEEDSPSHIK 240

Db 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLGGEEDSPSHIK 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 5  
US-09-361-736B-10  
; Sequence 10, Application US/09361736B  
; Patent No. 6613877  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Human Stannocalcin-Alpha  
; FILE REFERENCE: PFI43PID1  
; CURRENT APPLICATION NUMBER: US/09/361,736B  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: 08/460,529  
; PRIOR FILING DATE: 1995-06-02  
; PRIOR APPLICATION NUMBER: PCT/ US94/13206  
; PRIOR FILING DATE: 1994-11-30  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: human  
US-09-361-736B-10

Query Match 100.0%; Score 1268; DB 4; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1,6e-136;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MLQNSAVLVLVISASATHEAQNDSVSPKSRVAAQNSAEVVRCLNSALQVGGCAFACL 60  
QY 61 ENSTCDTDGMYDICKSLYSAKFTDQGAFFVESLKCICANGVTSKVFLAIRRCSSTFORM 120  
Db 61 ENSTCDTDGMYDICKSLYSAKFTDQGAFFVESLKCICANGVTSKVFLAIRRCSSTFORM 120  
QY 121 IAEVQECISKLVNCSIAKRNPEALTEVVOLEPHNSNRYNRLVSLLECEDETVSTIRD 180  
Db 121 IAEVQECISKLVNCSIAKRNPEALTEVVOLEPHNSNRYNRLVSLLECEDETVSTIRD 180  
QY 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLGGEEDSPSHIK 240  
Db 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLGGEEDSPSHIK 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 6  
US-08-208-005C-5  
; Sequence 5, Application US/08208005C  
; Patent No. 5837498  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stannocalcin  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSER: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE

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Query Marckc 52.1%: Score 660.5; DB 2; Length 204;
Best Local Similarity 60.8%: Pred. No. 3,4e-67;
Matches 119; Conservative 38; Mismatches 37; Indels 1; Gaps 1

Cy 11 LVISASATHEADONDSVSPRKSRYVAQNSAEVYCLNSALQVCGAFACLENSTCTDGM 70
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Db 12 LVGTGATDTDPDEEA-SPRRARFSPNSPSVAVACINLGAALVGGTFACLENSTCTDGM 70
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Cy 71 YDIKSAFLVSAAKFDTQGAIFYKESLKCICANGVTSKYFLAIRCSTPORMIAVECEYS 130
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 HDICQLFHTIATENTQGTFFVKSRLCIANGVTSKYFQITRCGVFQRMISVQECYS 130
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Cy 131 KLVNYSIARNDPEAITVEVQLNFHPSNRYNRLVRSLLCEDEDTSTIRDSLMEKIGPM 190
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 RLIDCGVARSNPEAIGEYVQVPAFPNNRYSTLLQSLACDEETAVAVRAGLVARIGPDM 190
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Cy 191 ASLPHILOTDHCQ 204
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 191 ETLFOLLONKHCPQ 204
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
US-09-038-597A-5
Sequence 5, Application US/09038597A
Patent No. 5877290
GENERAL INFORMATION:
APPLICANT: OLSEN, ET AL.
TITLE OF INVENTION: Corpuscles of Stannius Protein,
TITLE OF INVENTION: Stannocalcin
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILTTILAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,597A
FILING DATE:
CLASSIFICATION:

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Query Match	52.1%;	Score 660.5;	DB 2;	Length 204;
Best Local Similarity	60.8%;	Pred. No. 3.4e-67;		
Matches 118;	Conservative 38;	Mismatches 37;	Indels 1;	Gaps 1.

1 RESULT 8 US-08-460-529B-9  
2 Sequence 9, Application US/08460529B  
3 Patent No. 5994103  
4 GENERAL INFORMATION:  
5 APPLICANT: OLSEN, ET AL.  
6 TITLE OF INVENTION: Human Staminalc1in-alpha  
7 NUMBER OF SEQUENCES: 10  
8 CORRESPONDENCE ADDRESS:  
9 ADDRESSEE: CARRELLA, BYRNE, BAIN, GILFILLAN,  
10 ADDRESSEE: CECCHI, STEWART & OLSTEIN  
11 STREET: 6 BECKER FARM ROAD  
12 CITY: ROSELAND  
13 STATE: NEW JERSEY  
14 COUNTRY: USA  
15 ZIP: 07068  
16  
17 COMPUTER READABLE FORM:  
18 MEDIUM TYPE: 3.5 INCH DISKETTE  
19 COMPUTER: IBM PS/2  
20 OPERATING SYSTEM: MS-DOS  
21 SOFTWARE: WORD PERFECT 5.1  
22 CURRENT APPLICATION DATA:  
23 Application Number: US/08/460,529B  
24 FILING DATE: June 2, 1995  
25  
26 CLASSIFICATION: 435  
27  
28 PRIOR APPLICATION DATA:  
29 Application Number: PCT/US94/13206  
30 FILING DATE: 10 NOV 1994  
31 ATTORNEY/AGENT INFORMATION:  
32 NAME: MULLINS, J.G.  
33 REGISTRATION NUMBER: 33,073  
34 REFERENCE/DOCKET NUMBER: 325800-334 (PFI43  
35 TELECOMMUNICATION INFORMATION:



TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 170 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-08-460-529B-9

Query Match 49.5%; Score 628; DB 2; Length 170;  
Best Local Similarity 66.5%; Pred. No. 1.3e-63;  
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

QY 28 SPRKSAVAQNSAEVYRCINSAIQVCGGAFACIENSTCDTDGMIDICKSFLYSAAKFDPTQ 87  
DB 1 SPTAFSASSPSDVARCINQALQVCGSAPACIDNSTCNTDGMHRCISFLHGAAPDPTQ 60  
QY 88 GKAFVSESICKTANGVTSTVPLAIRRSTFORMIAVEQECYSKLVNCSIAKRNPEATPE 147  
DB 61 GKTFFVESIKCINANGITSKYFLTRCSSFQKMSIVQECYSKLDLCSVAQSNPEAMGE 120  
QY 148 VVQLPNNFNSRRYNNRLVRSLLCEDTVAETIRDSLMEKIGPMNASLFIHL 197  
DB 121 VAQVPSQFPNRRYSTLLQSLTCTDEDTVEQVRAGLVSRLEPENGVLFIQLL 170

RESULT 9  
US-09-361-736B-9  
Sequence 9, Application US/09361736B  
Patent No. 6613877  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Human Staminalcain-Alpha  
FILE REFERENCE: FFI43P1D1  
CURRENT APPLICATION NUMBER: US/09/361,736B  
CURRENT FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: 08/460,529  
PRIOR FILING DATE: 1995-06-02  
PRIOR APPLICATION NUMBER: PCT/ US94/13206  
PRIOR FILING DATE: 1994-11-30  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 9  
LENGTH: 170  
TYPE: PRT  
ORGANISM: Anguilla australis  
US-09-361-736B-9

Query Match 49.5%; Score 628; DB 4; Length 170;  
Best Local Similarity 66.5%; Pred. No. 1.3e-63;  
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

QY 28 SPRKSAVAQNSAEVYRCINSAIQVCGGAFACIENSTCDTDGMIDICKSFLYSAAKFDPTQ 87  
DB 1 SPTAFSASSPSDVARCINQALQVCGSAPACIDNSTCNTDGMHRCISFLHGAAPDPTQ 60  
QY 88 GKAFVSESICKTANGVTSTVPLAIRRSTFORMIAVEQECYSKLVNCSIAKRNPEATPE 147  
DB 61 GKTFFVESIKCINANGITSKYFLTRCSSFQKMSIVQECYSKLDLCSVAQSNPEAMGE 120  
QY 148 VVQLPNNFNSRRYNNRLVRSLLCEDTVAETIRDSLMEKIGPMNASLFIHL 197  
DB 121 VAQVPSQFPNRRYSTLLQSLTCTDEDTVEQVRAGLVSRLEPENGVLFIQLL 170

RESULT 10  
US-08-831-132-14  
Sequence 14, Application US/08831132  
Patent No. 6008322  
GENERAL INFORMATION:  
APPLICANT: Kuestner, Rolf E.

APPLICANT: Conklin, Darrell C.  
APPLICANT: Lok, Si  
APPLICANT: Buddle, Michele  
APPLICANT: Downey, William  
TITLE OF INVENTION: STANNIOCALCIN-2  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zymogenetics, Inc.  
STREET: 1201 Baslake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/831,132  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sawislak, Deborah A.  
REGISTRATION NUMBER: 37,438  
REFERENCE/DOCKET NUMBER: 96-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6672  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 296 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-831-132-14

Query Match 28.0%; Score 354.5; DB 3; Length 296;  
Best Local Similarity 31.7%; Pred. No. 5.9e-32;  
Matches 85; Conservative 45; Mismatches 109; Indels 29; Gaps 5;

QY 7 VLVTVIVISASATHAEQNDVSP-----RKSPVAQNSAEVYRCINSAIQVCGGAFACIENSTCDTDGMIDICKSFLYSAAKFDPTQ 56  
DB 10 VTLALVF--ATLDPAGQDSTNPBEGPQDRSSQKGLSLQNTIMEIQHCLVNAAGDVGGV 67  
QY 57 FACLENSCTDGMIDICKSFLYSAAKFDPTQGAFAVESIKCIANGVTSTVPLAIRRST 116  
DB 68 FEFENNSCETIQGLHGIQMTFLHNAAGKFDQGSFIDALRCXHALRHKFGCISRKCPA 127  
QY 117 FORMIAVEQECYSKLVNCSIAKRNPEATPEVQLPNNFNSRRYNNRLVRSLLCEDTVAETIRDSLMEKIGPMNASLFIHL 176  
DB 128 IREWVFOQRRCYKHLQCSAQENVGIVEMHFKULLHEPVVDLVNLLTCTGEBVKE 187  
QY 177 TIRDSLMEKIGPMNASLFIHL-----CTDHCAGTHT---PRADFNRRRTNEPCKLKV 224  
DB 188 AVTRSVQAQCHQSQSGGLCSILSFCSTSMIQREPTLAPRHQPLADAAQSLRPHNRDTIDHLLT 247  
QY 225 LLRLNGEEDSPSHIK---RTSHESA 247  
DB 248 ANRGAKGGRGSKSHPNHARGRTGQSA 275

RESULT 11  
US-09-416-150-14  
Sequence 14, Application US/09416150  
Patent No. 6171822  
GENERAL INFORMATION:  
APPLICANT: Kuestner, Rolf E.  
APPLICANT: Conklin, Darrell C.  
Lok, Si  
Buddle, Michele  
Downey, William  
TITLE OF INVENTION: STANNIOCALCIN-2



Page 7

Query Match	27.9%	Score 354	DB 3	Length 302
Best Local Similarity	32.4%	Pred. No. 6	96-33	
Matches	83	Conservative	45	Mismatches 102; Indels 26; Gaps 4
Qy	5	LVLVLS-----AAATHEAE-QNDVSPPKRSRYLAQNSAEVYRCLSNALSQVCCGACFAC	60	
Db	12	LALVLAATPDPAAGTDAATNPPEGPORRSQOQGRISLONTAEIHCILVNAGDVCCGTECF	71	
Qy	61	ENSTCDDTDMYICKSFLYSAKFEPTQGAFKESLKCINAGVSKYFLAIRCSTFCPRM	120	
Db	72	ENNSCEIRGLHIGMTFLHNAGKFDAGCKSPIKDALCKAHALRHRFGCISRCRAIRM	131	
Qy	121	IAEVDCECKSLKAVCSIAKNEPEALTEVYQLPNHSRYNRLYRSLBEDDELYSTTFD	180	
Db	132	VSQLOQECYLRKDLCAAAQENTRYIVETIMHKDILLHEPVVDLVNLLTGTGEVEKEATH	191	
Qy	181	SLMEKLGPMNMSLFPIILQ-TDHCQATHRADPNRRRTNEPQK-----	222	
Db	192	SVQVCGEQWMSLCSILSPCTSAISLQKPTAPPEQPOVDRTKLSRAHNGBAGHNLPEPS	251	
Qy	223	KYLRLRLRGEDSPSH	238	
Db	252	KETGRCAKGRGSKSH	267	

Query Match	27.9%: Score 354; DB 4; Length 302;	Best Local Similarity 32.4%; Pred. No. 6,9e-32;	Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;
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Db	72 ENNSCEIRGHJGICMTPLHNAGKFDAGGKSPFKDALCKKHALHRRGCTSRKCPAIREM	131	
QY	121 IAEVQEECYKLVNCSTAKRNPEAITFEVOLPNHFSRYYNRILVRSLLCEDEDTVSTIRD	180	
Db	132 VSGQGRCCYIKHDKCAAAQENTRIYVEMIHFKDILLHEPYVDLVNLLLTGCEEVKEAITH	191	
QY	181 SLMEKIGIPNNASLFLHIQ-TDHCAGQTPRADFNRRFRNPEOKL-----	222	
Db	192 SVQVQCEQNNNGSLCSILISFCTSAIOKEPTAPPERQPOVDRTKLSRAHNGEAGHHLPBSS	251	
QY	223 KYLLRLRGEDSDPSH 238		
Db	252 RETGRGAKGERGSKSH 267		

Db	192	SVVOCCQCNWWSLCSILSFCSTSAIQKPTAPPEROQYDRTKLSRAHGEAGHLLPEPSS	251
Qy	223	KVLLRNLRGEEDSPSH	238
	:	:	:
Db	252	REYGRGAKGERGSKSH	267

Search completed: November 16, 2004, 10:00:53  
Job time : 40 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2004, 09:59:29 ; Search time 143 Seconds  
(without alignments)  
611.142 Million cell updates/sec

Title: US-09-703-350b-76

Perfect score: 1268  
Sequence: 1 MLQNSAVLLVLTASATHE.....NIRGEEDSPSHIKRTSESA 247

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 35381937 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
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  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
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  - 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
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  - 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
  - 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
  - 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
  - 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1268	100.0	247	9	US-09-840-989A-2
2	1268	100.0	247	9	US-09-361-736-10
3	1268	100.0	247	13	US-10-116-051-2
4	1268	100.0	247	14	US-10-177-293-441
5	1268	100.0	247	14	US-10-418-226-10
6	1268	100.0	247	14	US-10-465-572-18
7	1268	100.0	247	15	US-10-372-663-41
8	1268	100.0	247	17	US-10-614-990-2
9	937	73.9	276	9	US-09-925-300-1446
10	662.5	52.2	256	9	US-09-840-989A-3
11	662.5	52.2	256	17	US-10-614-990-3
12	660.5	52.1	204	13	US-10-116-051-10
13	628	49.5	170	9	US-09-361-736-9

14	628	49.5	170	14	US-10-418-226-9	Sequence 9, Appli
15	358	28.2	70	9	US-09-864-761-37770	Sequence 37770, A
16	354	27.9	302	9	US-09-193-881-23	Sequence 23, Appl
17	354	27.9	302	14	US-10-177-293-443	Sequence 443, App
18	354	27.9	302	14	US-10-338-395-23	Sequence 23, Appl
19	354	27.9	302	14	US-10-418-226-12	Sequence 12, Appl
20	354	27.9	302	14	US-10-364-889-4	Sequence 4, Appli
21	354	27.9	302	14	US-10-295-027-100	Sequence 100, App
22	354	27.9	302	15	US-10-173-999-80	Sequence 80, Appl
23	354	27.9	302	15	US-10-058-270A-22	Sequence 22, Appl
24	351.5	27.7	251	14	US-10-418-226-2	Sequence 2, Appli
25	333.5	26.3	9	9	US-09-361-736-2	Sequence 2, Appli
26	303	23.9	118	13	US-10-116-051-9	Sequence 9, Appli
27	95.5	7.5	299	15	US-10-282-122A-49895	Sequence 49895, A
28	94.5	7.5	415	17	US-10-425-115-320042	Sequence 320042,
29	92	7.3	1010	17	US-10-425-115-312927	Sequence 312927,
30	91	7.2	901	16	US-09-828-062-8	Sequence 8, Appli
31	91	7.2	901	16	US-10-768-511-8	Sequence 8, Appli
32	90.5	7.1	783	15	US-10-149-310-96	Sequence 96, Appl
33	90	7.1	281	11	US-09-873-278-172	Sequence 172, App
34	90	7.1	281	11	US-09-873-278-277	Sequence 277, App
35	90	7.1	331	15	US-10-264-049-2324	Sequence 2324, Ap
36	89.5	7.1	622	16	US-10-437-963-161551	Sequence 161551,
37	89.5	7.1	1123	15	US-10-282-122A-54827	Sequence 70581, A
38	89.5	7.1	10203	16	US-10-661-809-23	Sequence 320050,
39	89	7.0	201	17	US-10-425-115-320050	Sequence 23, Appl
40	89	7.0	431	17	US-10-425-115-285165	Sequence 285165,
41	86	6.8	401	15	US-10-425-114-63193	Sequence 63193, A
42	86	6.8	470	15	US-10-282-122A-54827	Sequence 54827, A
43	86	6.8	529	17	US-10-289-762-299	Sequence 299, App
44	86	6.8	529	17	US-10-425-115-320053	Sequence 320053,
45	85.5	6.7	564	15	US-10-424-599-272057	Sequence 272057,

ALIGNMENTS

RESULT 1  
US-09-840-989A-2  
; Sequence 2, Application US/09840989A  
; Patent No. US20020042372A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen et al.  
; TITLE OF INVENTION: Stannocalcin Polynucleotides, Polypeptides, and Methods Based The  
; FILE REFERENCE: PFI0892  
; CURRENT APPLICATION NUMBER: US/09/840, 989A  
; CURRENT FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: PCT/US00/29432  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,740  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-840-989A-2

Query Match 100.0%; Score 1268; DB 9; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9, 9e-121; Indels 0; Gaps 0;  
Matches 247; Conservative 0; Mismatches 0;

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Db 1 MLQNSAVLLVLTASATHEAONDSVSPKSRVAQNSAEVVRCLNSALQVGGAFACL 60

Cy 61 ENSICDDTDGMDICKSLTYSAAKFDITGGKAFVHESLKCINAGVTSKFLAIRGSTQRM 120  
Db 61 ENSICDDTDGMDICKSLTYSAAKFDITGGKAFVHESLKCINAGVTSKFLAIRGSTQRM 120

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Db 121 IAEVDEECYSKLVNCSIAKRNPEALTEVQLPNHSNRYNRLVSLLECEDEDTYSTIRD 180  
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Db 181 SLMEKIGPMNASLPHILQTDHCAQTHPRADFNRRTNEPQKLVLLRNLRGGEEDSPSHIK 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

## RESULT 2

US-09-361-736-10  
; Sequence 10, Application US/09361736  
; Patent No. US20020102634A1  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Human Stannocalcin-alpha  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAPILLA, BYRN, BAIN, GILFILLAN,  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/361,736  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/460,529  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MILLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-334 (PFI43)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1744  
; TELEFAX: 201-994-1700  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 247 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
US-09-361-736-10

Query Match 100.0%; Score 1268; DB 9; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9,9e-121;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 181 SLMEKIGPMNASLPHILQTDHCAQTHPRADFNRRTNEPQKLVLLRNLRGGEEDSPSHIK 240  
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QY 241 RTSHESA 247  
Db 241 RTSHESA 247

## RESULT 3

US-10-116-051-2  
; Sequence 2, Application US/10116051  
; Publication No. US20020146791A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen et al.  
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNICALCIN  
; FILE REFERENCE: PFI08PDI01  
; CURRENT APPLICATION NUMBER: US/10/116,051  
; CURRENT FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 09/312,610  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 08/431,117  
; PRIOR FILING DATE: 1995-04-28  
; PRIOR APPLICATION NUMBER: 08/208,005  
; PRIOR FILING DATE: 1994-03-08  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-116-051-2

Query Match 100.0%; Score 1268; DB 13; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9,9e-121;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 RTSHESA 247  
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## RESULT 4

US-10-177-293-441  
; Sequence 441, Application US/10177293  
; Publication No. US20030124128A1  
; GENERAL INFORMATION:  
; APPLICANT: Lillie, James  
; APPLICANT: Galt, Karen  
; APPLICANT: Zhao, Xumei  
; APPLICANT: Ganuwaipu, Manjula  
; APPLICANT: Kamakkar, Shubhangi  
; APPLICANT: Mertens, Maureen  
; APPLICANT: Myer, Vic  
; APPLICANT: Wang, Youzhen  
; APPLICANT: Xu, Yongyao  
; APPLICANT: Hoersch, Sebastian  
; APPLICANT: Morahan, John  
; APPLICANT: Meyers, Rachel E.

```
/ APPLICANT: Bast Jr., Robert C.
/ APPLICANT: Hortobagyi, Gabriel N.
/ APPLICANT: Pusztai, Lajos
/ APPLICANT: Meric, Funda
/ APPLICANT: Sahin, Aysegul
/ APPLICANT: Mills, Gordon B.
/ TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
/ FILE REFERENCE: PREVENTION, AND THERAPY OF BREAST CANCER
/ FILE REFERENCE: MRI-038
/ CURRENT APPLICATION NUMBER: US/10/177,293
/ CURRENT FILING DATE: 2002-06-21
/ PRIOR APPLICATION NUMBER: US 60/299,887
/ PRIOR FILING DATE: 2001-06-21
/ PRIOR APPLICATION NUMBER: US 60/301,572
/ PRIOR FILING DATE: 2001-06-27
/ PRIOR APPLICATION NUMBER: US 60/306,501
/ PRIOR FILING DATE: 2001-07-18
/ PRIOR APPLICATION NUMBER: US 60/325,002
/ PRIOR FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: US 60/362,585
/ PRIOR FILING DATE: 2002-03-05
/ PRIOR APPLICATION NUMBER: US 60/xxx,xxx
/ PRIOR FILING DATE: 2002-05-14
/ NUMBER OF SEQ ID NOS: 506
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 441
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/ TYPE: PRT
/ ORGANISM: Homo sapiens
us-10-177-293-441
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Query Match      100.0%; Score 1268; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.9e-121;
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DB 61 ENSTCDDTDMGYDICKSFLYSAAKFDTOGKAFVKSILKCIANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDEDTVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADPNRRRTNEPQKLKVLNNLNGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADPNRRRTNEPQKLKVLNNLNGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247
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RESULT 5
us-10-418-226-10
/ Sequence 10, Application US/10418226
/ Publication No. US2003018163A1
/ GENERAL INFORMATION:
/ APPLICANT: Human Genome Sciences, Inc.
/ TITLE OF INVENTION: Human Stemmicalcin-Alpha
/ FILE REFERENCE: PFI43P1D2
/ CURRENT APPLICATION NUMBER: US/10/418,226
/ CURRENT FILING DATE: 2003-04-18
/ PRIOR APPLICATION NUMBER: 09/361,736
/ PRIOR FILING DATE: 1999-07-28
/ PRIOR APPLICATION NUMBER: 08/460,529
/ PRIOR FILING DATE: 1995-06-02
/ PRIOR APPLICATION NUMBER: PCT/ US94/13206
/ PRIOR FILING DATE: 1994-11-30
/ NUMBER OF SEQ ID NOS: 12
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/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 10
/ LENGTH: 247
/ TYPE: PRT
/ ORGANISM: human
us-10-418-226-10
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Query Match      100.0%; Score 1268; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.9e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MLONSAVLLVIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVGGGAFACL 60
DB 1 MLONSAVLLVIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVGGGAFACL 60
QY 61 ENSTCDDTDMGYDICKSFLYSAAKFDTOGKAFVKSILKCIANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDDTDMGYDICKSFLYSAAKFDTOGKAFVKSILKCIANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDEDTVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADPNRRRTNEPQKLKVLNNLNGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADPNRRRTNEPQKLKVLNNLNGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247
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RESULT 6
us-10-465-572-18
/ Sequence 18, Application US/10465572
/ Publication No. US20030207840A1
/ GENERAL INFORMATION:
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/ APPLICANT: Riggin, Gregory
/ APPLICANT: Lal, Anita
/ TITLE OF INVENTION: GENES INDUCED BY HYPOXIA
/ FILE REFERENCE: 000250.00012
/ CURRENT APPLICATION NUMBER: US/10/465,572
/ CURRENT FILING DATE: 2003-06-20
/ PRIOR APPLICATION NUMBER: US/10/201,642
/ PRIOR FILING DATE: 2002-07-24
/ PRIOR APPLICATION NUMBER: 60/307,600
/ PRIOR FILING DATE: 2001-07-26
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 18
/ LENGTH: 247
/ TYPE: PRT
/ ORGANISM: Homo sapiens
us-10-465-572-18
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Query Match      100.0%; Score 1268; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.9e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MLONSAVLLVIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVGGGAFACL 60
QY 61 ENSTCDDTDMGYDICKSFLYSAAKFDTOGKAFVKSILKCIANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDDTDMGYDICKSFLYSAAKFDTOGKAFVKSILKCIANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDEDTVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADPNRRRTNEPQKLKVLNNLNGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADPNRRRTNEPQKLKVLNNLNGEEDSPSHIK 240
```

Db 181 SLMEKIGPMNASLFIHLQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLGGEEDSPSHIK 240  
QY 241 RTSHESA 247  
241 RTSHESA 247

## RESULT 7

US-10-372-683-41  
; Sequence 41, Application US/10372683  
; Publication No. US20040009171A1  
; GENERAL INFORMATION:  
; APPLICANT: GERRITSEN, MARY E.  
; APPLICANT: PEALE JR., FRANKLIN V.  
; APPLICANT: WU, THOMAS D.  
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA  
; FILE REFERENCE: P1928R1P1  
; CURRENT APPLICATION NUMBER: US/10/372,683  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: US 10/271,690  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: US 60/344,534  
; PRIOR FILING DATE: 2001-10-18  
; NUMBER OF SEQ ID NOS: 49  
; SEQ ID NO 41  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-372-683-41

Query Match 100.0%; Score 1268; DB 15; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9.9e-121;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTONSAVLVLVIVISASATHEAEONDSVSPKRSRVAAQNSAEVYRCINSLAQVGCAPACT 60  
Db 1 MTONSAVLVLVIVISASATHEAEONDSVSPKRSRVAAQNSAEVYRCINSLAQVGCAPACT 60  
QY 61 ENSTCDTDGMYDICKSFLYSAAKFTDQKAFVKSILCIANGVTSKVFLAIRRCSFTQRM 120  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFTDQKAFVKSILCIANGVTSKVFLAIRRCSFTQRM 120  
QY 121 IAEVQECYSKLVNCSIAKRNPEALTEVQLPNHFENRYNRLVSLSCDEDTYSTIRD 180  
Db 121 IAEVQECYSKLVNCSIAKRNPEALTEVQLPNHFENRYNRLVSLSCDEDTYSTIRD 180  
QY 181 SLMEKIGPMNASLFIHLQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLGGEEDSPSHIK 240  
Db 181 SLMEKIGPMNASLFIHLQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLGGEEDSPSHIK 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

## RESULT 8

US-10-614-990-2  
; Sequence 2, Application US/10614990  
; Publication No. US20040138658A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen et al.  
; TITLE OF INVENTION: Stannocalcin Polynucleotides, Polypeptides, and Methods Based Th  
; FILE REFERENCE: P108P2  
; CURRENT APPLICATION NUMBER: US/10/614,990  
; CURRENT FILING DATE: 2003-07-09  
; PRIOR APPLICATION NUMBER: US/09/840,989A  
; PRIOR FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: PCT/US00/29432  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,740  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-614-990-2

Query Match 100.0%; Score 1268; DB 17; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9.9e-121;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTONSAVLVLVIVISASATHEAEONDSVSPKRSRVAAQNSAEVYRCINSLAQVGCAPACT 60  
Db 1 MTONSAVLVLVIVISASATHEAEONDSVSPKRSRVAAQNSAEVYRCINSLAQVGCAPACT 60  
QY 61 ENSTCDTDGMYDICKSFLYSAAKFTDQKAFVKSILCIANGVTSKVFLAIRRCSFTQRM 120  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFTDQKAFVKSILCIANGVTSKVFLAIRRCSFTQRM 120  
QY 121 IAEVQECYSKLVNCSIAKRNPEALTEVQLPNHFENRYNRLVSLSCDEDTYSTIRD 180  
Db 121 IAEVQECYSKLVNCSIAKRNPEALTEVQLPNHFENRYNRLVSLSCDEDTYSTIRD 180  
QY 181 SLMEKIGPMNASLFIHLQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLGGEEDSPSHIK 240  
Db 181 SLMEKIGPMNASLFIHLQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLGGEEDSPSHIK 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

## RESULT 9

US-09-925-300-1426  
; Sequence 1426, Application US/09925300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen,  
; APPLICANT: Steve Ruben  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: P4101  
; CURRENT APPLICATION NUMBER: US/09/925,300  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05988  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1890  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1426  
; LENGTH: 276  
; TYPE: PRT  
; ORGANISM: Homo sapiens

; FEATURES:  
; NAME/KEY: SITE  
; LOCATION: (43)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (273)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (275)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-300-1426

Query Match 73.9%; Score 937; DB 9; Length 276;  
Best Local Similarity 99.5%; Pred. No. 6.6e-87;  
Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTONSAVLVLVIVISASATHEAEONDSVSPKRSRVAAQNSAEVYRCINSLAQVGCAPACT 60  
Db 89 MTONSAVLVLVIVISASATHEAEONDSVSPKRSRVAAQNSAEVYRCINSLAQVGCAPACT 148  
QY 61 ENSTCDTDGMYDICKSFLYSAAKFTDQKAFVKSILCIANGVTSKVFLAIRRCSFTQRM 120



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us-09-703-350b-76.rapb

Page 5

Db	149	ENSTCDDIDGMWDICKSFLYSAKPEDTQSKAVKSLKIANGVTSKPYLAIRRCSSTPQRM	208
QY	121	IAEVOEECYSLVNTCSIAKRNPEAITVEVQLPNHFSNRYYNRLVSLLECCEDFTVSTIRD	180
Db	209	IAEVOEECYSLVNTCSIAKRNPEAITVEVQLPNHFSNRYYNRLVSLLECCEDFTVSTIRD	268
QY	181	SLMEXI	186
Db	269	SLMEXI	274

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RESULT 10
US-09-840-989A-3
; Sequence 3, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Steamlocalcain Polynucleotides, Polypeptides, and Methods Based Th
; FILE REFERENCE: PF10882
; CURRENT APPLICATION NUMBER: US/09/840, 989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Oncorhynchus kisutch
; US-09-840-989A-3

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[illegible]

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RESULT 11
US-10-614-990-3
; Sequence 3, Application US/10614990
; Publication No. US20040198658A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stannocalcin Polynucleotides, Polypeptides, and Methods Based Th
; FILE REFERENCE: PFI08P2
; CURRENT APPLICATION NUMBER: US/10/614,990
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/840,989A
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRF
; ORGANISM: Oncorhynchus kisutch
US-10-614-990-3

Query Match      52.2%   Score 662.5; DB 17; Length 256;
Best Local Similarity 53.4%   Pred. No. 66-59;
Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;

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Qy 11 LVISASATHEAONDVSPKRSRYAONSAEVRCLNSALQVGGCAFIENSTCDTDGM 70
   | : : : : :
Db 12 LVIGTATPTPDDEEA -SPRRARSSNSPSDVARCINLGAALVGGTFACIENSTCDTDGM 70
   | : : : : :
Qy 71 YDIKSTLYSNAKDDTGGKAPVAKESLKCINAGTYSKFLAIRRSTQRMIAEVOEBCYS 130
   | : : : : :
Db 71 HDIQLEFHFAATFNTGKTFVESLFCINAGTYSKFTQTRRGQVRQRMISEVOEBCYS 130
   | : : : : :
Qy 131 KLANVSIAKNPEALTEVVOLEJNFNSRYNRLVRSLLCEDEDPTSTIRDSLEKTIIPNM 190
   | : : : : :
Db 131 RLIDICGVARNSPEALIGEVQVPAAHFPRYYSTLLQSLACDEBEVAVAVRAGLVARLGPDM 190
   | : : : : :
Qy 191 ASLPHIITQDCAQTHPRADPN-----RRKTNEPQKLVLRINLRGEDEDSH 229
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Db 191 ETLEQQLQNKHCPCGNSQNGNSADAGRMWGPSPSPFKI -QPSRGSD -PTH 241
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RESULT 12
US-10-116-051-10
; Sequence 10, Application US/10116051
; Publication No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
; FILE REFERENCE: PF108PIDICI
; CURRENT APPLICATION NUMBER: US/10/116,051
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/312,610
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 08/431,117
; PRIOR FILING DATE: 1995-04-28
; PRIOR APPLICATION NUMBER: 08/208,005
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Oncorhynchus kisutch
US-10-116-051-10

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Query Match	52.1% ; Score 660.5 ; DB 13 ; Length 204 ;
Best Local Similarity	60.8% ; Pred. No. 7e-59 ;
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Qy	11 LVYISAKTHAEONDSVSPKRSRAAONSAAYVRCLNSALQVGGAFACLENSTCTDDGM 70
Db	12 LVIGTAATFTPIDPEEA-SPPRARSSNSPDVAACNLGALAVGGTFAACLENSTCTDDGM 70
Qy	71 YDICKSFLVSAAKFTDTGKAFVKESELKCIANGVTSKYFLAIRCSTFORMIAEVOEBCYS 130
Db	71 HDICOLFHTFAATFNTQGTFFVESLRCIANGVTSKFTQIRRCGVFORMISEVOEBCYS 130
Qy	131 KLVNCSFAKNSEPAITFVQLPNNFSRRYNNRLVRSLLCEDCEPVSFTIRSLIMEKIGPNM 190
Db	131 RLDDCGVARGNSEPAISGVQVPAAHFPKRYYSTLLQSLACDEDEIVAAVVRAGLVARLEPDM 190
Qy	191 ASLPHILQTDHCAQ 204
Db	191 ETEFQLLNKRCPCQ 204

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; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Anguilla australis
US-10-418-226-9

Query Match      49.5%;   Score 628; DB 14;   Length 170;
Best Local Similarity 66.5%;   Pred. No. 1,1e-55;
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

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Db      1  SPETAFASASSPEDVARCLNGALQVCGSAFACLDNSTCNTDMEHICRSFLHGAAKFDQ 60

Cy      88  GKAFVRESLCKLNGVTSKVPFLAIRGCSFQGMIAVEQEECKSKNVSIAKNEALTE 147
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      61  GKPFVRESLCKLNGVTSKVPFLTIRGCSFQGMISVEQEECKSKLDLSVAQNSPEALGE 120

Cy      148  VVQVPHNPSNRYYNRLVRSLLTECEDVTSYTIKDSIMKIGPMASLPHIL 197
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      121  VAVQPSQCFPNRYSTLLQSLLTCTDEDTVEQVRAGLVSRLEPMGVLPOLL 170

RESULT 15
US-09-664-761-37770
; Sequence 37770, Application US/09664761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37770
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC012119.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
; OTHER INFORMATION: SWISSPROT HIT: P52823, EVALUATE 3.00e-35
; OTHER INFORMATION: EST_HUMAN HIT: AW954342.1, EVALUATE 3.00e-34
US-09-864-761-37770
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Query Match      28.2%; Score 358; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      88 GRAFVESIKCIANGVTSKVFLAIRRCSTFORMIAVEQECYKLVCSIAKNDEPAITE 147
Db      1 GRAFVESIKCIANGVTSKVFLAIRRCSTFORMIAVEQECYKLVCSIAKNDEPAITE 60

QY      148 VVQLPNHFSN 157
Db      61 VVQLPNHFSN 70
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Search completed: November 16, 2004, 10:11.40  
Job time : 144 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 09:37:33 ; Search time 40 Seconds

(without alignments)  
594.139 Million cell updates/sec

Title: US-09-703-350b-76

Sequence: 1 MLQNSAVLLVVISASATHE.....MLRGSEDSPIKRTSHESA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	680.5	53.7	263	2	stannocalcin prec
2	662.5	52.2	256	2	stannocalcin - co
3	354	27.9	302	2	stannocalcin homo
4	150	11.8	40	2	teleocalcin - coho
5	149	11.8	40	2	teleocalcin - sock
6	123	9.7	33	2	teleocalcin - rain
7	102	8.0	473	2	hypothetical prote
8	94	7.4	1105	2	hypothetical compl
9	90.5	7.1	289	2	hypothetical prote
10	90.5	7.1	783	2	probable regulator
11	89.5	7.1	1126	2	ubiquitin-protein
12	89	7.0	305	2	peroxidase (EC 1.1
13	88	6.9	473	2	hypothetical prote
14	87.5	6.9	1465	2	DNA-directed DNA p
15	86	6.8	470	2	hypothetical prote
16	86	6.8	470	2	Mg++ transporter (
17	86	6.8	510	2	hypothetical prote
18	86	6.8	556	2	probable membrane
19	86	6.8	581	2	conserved hypothet
20	83	6.5	250	2	hypothetical prote
21	83	6.5	250	2	hypothetical prote
22	83	6.5	365	2	hypothetical prote
23	83	6.5	1093	2	hypothetical prote
24	83	6.5	1094	2	hypothetical prote
25	82.5	6.5	869	2	protein C43G2.2 (1
26	82.5	6.5	1483	2	hypothetical prote
27	82.5	6.5	1757	2	hypothetical prote
28	82.5	6.5	2335	2	probable phosphati
29	82.5	6.5	2535	2	hypothetical prote

30	82	6.5	815	2	G72209	conserved hypothet
31	82	6.5	925	2	T01384	hypothetical prote
32	81.5	6.4	463	2	T15416	hypothetical prote
33	81.5	6.4	549	2	F64640	conserved hypothet
34	81.5	6.4	708	1	TFPBL	lactotransferrin p
35	81	6.4	358	2	S76692	hypothetical prote
36	81	6.4	720	2	UC5131	glycosyltransferas
37	81	6.4	1375	2	T18961	FAB1 protein homol
38	81	6.4	4377	2	A55575	ankyrin 3, long sp
39	80	6.3	281	2	H84720	probable endonucle
40	80	6.3	509	1	VGNVPC	major envelope gly
41	80	6.3	509	2	T10395	protein gp64 - Org
42	80	6.3	985	2	T00633	Ca2+-transporting
43	80	6.3	998	2	T52581	Ca2+-transporting
44	80	6.3	1178	2	S54073	probable membrane
45	80	6.3	1188	2	T46608	zinc finger protei

ALIGNMENTS

RESULT 1  
A54648  
stannocalcin precursor - Australian eel  
N|Alterate names: Stannius corpuscle secretory protein  
C|Species: Anguilla australis (Australian eel)  
C|Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #text\_change 09-Jul-2004  
C|Accession: A54648  
R|Butkus, A.; Roche, P.J.; Fernley, R.T.; Haralambidis, J.; Penschow, J.D.; Ryan, G.B.; J  
Mol. Cell. Endocrinol. 54, 123-133, 1987  
A|Title: Purification and cloning of a corpuscles of Stannius protein from Anguilla austi  
A|Reference number: A54648; MUID:88083961; PMID:3319739  
A|Accession: A54648  
A|Status: preliminary  
A|Molecule type: mRNA  
A|Residues: 1-263 <BUT>  
A|Cross-references: UNIPROT:P18301  
F|1-17|Domain: signal sequence #status predicted <SIG>  
F|18-263|Product: stannocalcin #status predicted <MAT>

Query Match 53.7%; Score 680.5; DB 2; Length 263;  
Best Local Similarity 61.4%; Pred. No. 3.7e-51;  
Matches 124; Conservative 41; Mismatches 36; Indels 1; Gaps 1;  
  
QY 1 MLQNSAVLLVVISASATHEAQNDSVPRKSRVAQNSAEVVCUNSAIOVGGAFACL 60  
DB 1 MLRNSGLITLVLTVAAYEDSEPLSPTRPFSASSPDVARCLNGALQVGSAPACL 59  
QY 61 ENSTCDTDDGMYDICKSFYLSAKFDTOGKAFFVESLKCICANGVTSKVFLAIRCSIFQRM 120  
DB 60 DNSTCNTDGMHEILRSFLHGAKFDTOGKTFVESLKCICANGITRSKVFILTRCSSFQKM 119  
QY 121 IAEVQEECYKLANCSIAKRNPEAITVVDLPNHFSTRYNNRLVRSLLCEDDEDVSTRD 180  
DB 120 ISEVQEECYKCLDSCVAQNPBEAMGEVAQVPSQPRRYVSTLLQSLTDCDEDVQVRA 179  
QY 181 SLMEKIGPNMASLPHILOTDHC 202  
DB 180 GLVSRLEPEMGVLPOLLQTRAC 201  
  
RESULT 2  
151197  
stannocalcin - coho salmon  
C|Species: Oncorhynchus kisutch (coho salmon)  
C|Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C|Accession: 151197  
R|Wagner, G.F.; Dimattia, G.E.; Davie, J.R.; Copp, D.H.; Frissen, H.G.  
Mol. Cell. Endocrinol. 90, 7-15, 1992  
A|Title: Molecular cloning and cDNA sequence analysis of coho salmon stannocalcin.  
A|Reference number: 151197; MUID:93246046; PMID:1363790  
A|Accession: 151197  
A|Status: preliminary; translated from GB/EMBL/DBD

[illegible][illegible]

RESULT 7  
T04799  
hypothetical protein F10M23.100 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T04799  
R:Bevan, M.; Lecharny, A.; Chefdor, F.; Krivitzky, M.; Kreis, M.; Hohenisel, J.; Mewes, H.  
submitted to the Protein Sequence Database, February 1999  
A:Reference number: Z15385  
A:Accession: T04799  
A:Molecule type: DNA  
A:Residues: 1-473 <BEV>  
A:Cross-references: UNIPROT:Q95Z16; EMBL:AL035440  
A:Experimental source: cultivar Columbia; BAC clone F10M23  
C:Genetics:  
A:Map position: 4  
A:Introns: 24/3; 184/3; 256/3; 308/3; 412/3  
A:Note: F10M23.100

Query Match 8.0%; Score 102; DB 2; Length 473;  
Best Local Similarity 21.0%; Pred. No. 0.5;  
Matches 50; Conservative 43; Mismatches 67; Indels 78; Gaps 11;

QY 26 SVSPKSRVAQNSAVRCLNSALQVGGAFACLENSCTD---DGMVDCSKF-LYS 80  
DB 50 NVYKKKVVBLAAKSRRLDQLTSD-----ATVELSNLTALGKSYTIDICDSMSLFP 100  
QY 81 AAKFTDQKAFVYESLKCTA-----NG-- 102  
DB 101 LQPDKTSGR--IKQSLAIPALPQLQWQKERNVAFSVQSIQKICETINGGIANP 158  
QY 103 VTSKYFLAIRCSCTFGMTAEVQECYKLT-----NVCSIAKRN-PEATTEV-- 148  
DB 159 VVDETLSTKRLDDFQKLOELQKSDRLQKVLFEVSTVHDLCAVLRDPFSTYTEVAP 218  
QY 149 -----VQLPNHFSSRYNNRLVRSLLCEDPTVSTIRSLMEKIGPMNASLFHLLQT 199  
DB 219 SLDEANGVQTKS-ISNETIARLAKTVLTKEDKMKRLK--LQELATQLTDLIMLMDT 273

RESULT 8  
T18295  
Ap-3 adaptor complex beta3 chain - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T18295  
R:Feng, L.; Seymour, A.B.; Jiang, S.Y.; To, A.; Feden, A.A.; Novak, E.K.; Zhen, L.; Rust  
Hum. Mol. Genet. 8, 323-330, 1999  
A:Title: The beta3 subunit gene (Ap3b1) of the Ap-3 adaptor complex is altered in the m  
A:Reference number: Z18864; MIMD:99135912; PMID:9931340  
A:Accession: T18295  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1105 <FEN>  
A:Cross-references: UNIPROT:Q921T1; EMBL:AF103809; NID:93885987; PID:93885988; PIDN:AACT  
A:Experimental source: strain C3H/HeJ  
C:Genetics:  
A:Gene: Ap3b1  
A:Map position: 13

Query Match 7.4%; Score 94; DB 2; Length 1105;  
Best Local Similarity 21.2%; Pred. No. 6.7;  
Matches 55; Conservative 40; Mismatches 104; Indels 60; Gaps 11;

QY 1 MTQNSAVLLVIVISATSEAEONDSVSPKSRVAQNSAEVRCNSALQVGGAFAC 60  
DB 308 LQSRVAAVVMVAQLYWH-----ISPKSE--AGVTSKSLVRLRSREVOYIVLONI 358  
QY 61 ENSTCDDTDGMYD-ICSPFLYSAAKFTDQKAFVYESLKICANGVTSKVF----- 109  
DB 359 ATMSIRKGMFEYLSKF-YVRSSTDPTMTIKTLKELITVLAEANITSLIREFCYVRSQ 417

QY 110 -----AIRRCSTFORMIAEVEECYSKLNVCISIAKNPEATE---VQLPNHS 156  
DB 418 DKQPAATITQIGRCAT---SISEFTETCFNGL-VCLLSNRDEIVAESVYVVKLLQWQ 473  
QY 157 NRYNNRLVRSLE-CEDDTVSTIRDSLMEXIGPMNASLFHLLQDHCAGQHPADFNRR 215  
DB 474 PAQGEITIRHAKLDSITVPVAPASITLMIGEN-----CERVPKIA----- 515  
QY 216 TNEPQKLVLRNLGSEED 234  
DB 516 ---PDVIRKMAKSFSEDD 531

RESULT 9  
T50776  
hypothetical protein [imported] - Vitis vinifera  
C:Species: Vitis vinifera  
C>Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 09-Jul-2004  
C:Accession: T50776  
R:Matsumoto, S.; Dry, I.B.; Thomas, M.  
DNA Seq. 8, 109-112, 1997  
A:Title: Nucleotide sequence of grapevine (Vitis vinifera) cDNA similar to SNAP proteins.  
A:Reference number: Z25233  
A:Accession: T50776  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-289 <MAT>  
A:Cross-references: UNIPROT:P93798; EMBL:AB001375; PIDN:BA019246.1  
A:Experimental source: strain Shiraz

Query Match 7.1%; Score 90.5; DB 2; Length 289;  
Best Local Similarity 19.9%; Pred. No. 2.7;  
Matches 41; Conservative 33; Mismatches 95; Indels 37; Gaps 5;

QY 8 LTVIVIASATHEAEONDSVSPKSRVAQNSAEVRCNSALQVGGAFACLENSCTD 67  
DB 59 LSTVIGSDSGHEAAQ--AYADAGHCYKTSAAEALICLQD-----ALFLDNGRFNM 110  
QY 68 DG-----MYDICKSFLYSAAKFTDQKAFVYESLKICANGVTSKVFIAIRRCSTFOR 119  
DB 111 AGKYKKEIAELVEQNFQEQAIYFERKADIVQSEEAATTANQCAKVAQFAAQLEQYOK 170  
QY 120 MIAEVEECYSKLN-----VCISIAKNPEATEVQQL-----PNHFSNR 158  
DB 171 ALQIVEDIGRPSLNNNLLKGVKGLHNLAGICQCKGDVVAITVALDRYQEMDPTBSGTR 230  
QY 159 YNNRLVRSLECEDPTVSTIRSLME 184  
DB 231 EYKLLVLAQVDEVDVVKFTDAVKE 256

RESULT 10  
T38690  
probable regulatory protein - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 16-Aug-2004  
C:Accession: T38690  
R:Brown, D.; Churcher, C.M.; Wood, V.; Bartell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z21805  
A:Accession: T38690  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-783 <BRO>  
A:Cross-references: UNIPROT:Q14130; EMBL:Z69568; PIDN:CAB16735.1; GSPDB:GN00066; SPDB:SP7  
A:Experimental source: strain 972n; cosmid c3c7  
C:Genetics:  
A:Gene: SPDB:SPAC37.04  
A:Map position: 1  
C:Superfamily: GAL4 zinc binuclear cluster homology  
F.35-71/Domain: GAL4 zinc binuclear cluster homology <GLA>

Query Match 7.1%; Score 90.5; DB 2; Length 783;  
 Best Local Similarity 23.3%; Pred. No. 9;  
 Matches 56; Conservative 34; Mismatches 87; Indels 63; Gaps 12;

QY 10 VIVISASATHEAEONDSVSPKRSRV-----AAONSAEVRCLNSALQVCGCAF-----57  
 DB 535 IIMSRPVLHKMKAKNSPRVDRINEDCIIARHLISVHLQNHSLQSCSFEDNYVT 594  
 QY 58 -----ACLENSTCDTGMVYDICKSFYSAKFPDQKAFVKSJLCT-----99  
 DB 595 FSSALVLLHCY-TEPCEDD---DIAMQYVSGALDYMEGNMAKQACARVIRLPDAHLKG 650  
 QY 100 ----ANGVSKY-FLAIRRCSTFORMIAEVQ-----EEGYSKLVNCSIAKRPALTEVV 149  
 DB 651 AASDNGNTSGSGFMA-----WQKRIEVSADKDEPKLMSYKNSIGGGRNSNLTENA 704  
 QY 150 QLPNHSNRYNR-----LVRSLECEDETVSTRDSIMEXIGPMA---SLPHILOTD 200  
 DB 705 NIGADVVS--FFPDTDTSPILDSKLDLLEKFASTLDPI--KTPDLANDSILANWANTD 760

RESULT 11  
 T01491  
 ubiquitin-protein ligase homolog F1707.15 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
 C:Accession: T01491  
 R:Vysotskaya, V.S.; Schwartz, J.R.; Tortum, M.; Yu, G.; Khan, A.; Ojil, O.; Liu, S.; Li, R.; Vysotskaya, V.S.; Palm, C.O.; Shim, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N.  
 Submitted to the EMBL Data Library, June 1998  
 A:Description: Arabidopsis thaliana chromosome 1 BAC F1707 sequence.  
 A:Reference number: 214334  
 A:Accession: T01491  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1126 <VYS>  
 A:Cross-references: UNIPROT:Q64605; EMBL:AC003671; NID:G2833627; PID:G3176690; GSPDB:GNC  
 C:Experimental source: cultivar Columbia  
 C:Genetics:  
 A:Gene: ARSP:F1707.15  
 A:Map position: 1  
 A:Intons: 118/3; 224/1; 373/3; 457/2; 826/3; 875/3; 902/3; 1057/3; 1093/2  
 F:756-1120/Domain: ubiquitin-protein ligase homology <DBI>

Query Match 7.1%; Score 89.5; DB 2; Length 1126;  
 Best Local Similarity 22.1%; Pred. No. 17;  
 Matches 46; Conservative 39; Mismatches 76; Indels 47; Gaps 8;

QY 14 SASATHEAEONDSVSPKRSRVAAQNSAEVVRCLNSALQVCGCAFLENSTCD-----66  
 DB 412 SSETQKDAESELGVARRK-----NCAEL--YNIFLQLP-----OSDLCNLCMLQY 455  
 QY 67 ----TDCMYICKSFYSAKFPDQKAFVKSJLCTCIANGVSKYFLAIRRCSTFORMIAE 123  
 DB 456 EGLSDIKYSLAGEVYLKLAADVTRHKFTKELSELASLSSTVRVALTLSTQKM--512  
 QY 124 VOEECYSKLVNCSIAKRPALTEVVQLPNHSNRYNRVLVRSLECEDETVSTR-----179  
 DB 513 -----SQNTCSMA--CASILRVLYQVLSLSTIDSDNVTGTDRETQDEGNINQGLKV 562  
 QY 180 --DSLMEKIGPMA--PHILOTDHCAQT 205  
 DB 563 ALFPLWQELGQCIS--MTBLQDHTAAT 588

RESULT 12  
 T08121  
 peroxidase (EC 1.11.1.7) - flax (fragment)  
 C:Species: Linum usitatissimum (flax)  
 C:Date: 21-May-1999 #sequence\_revision 21-May-1999 #text\_change 09-Jul-2004  
 C:Accession: T08121  
 R:Omann, F.; Tysen, H.  
 Submitted to the EMBL Data Library, February 1998

A:Description: cDNA sequence of a basic peroxidase (FLXPER4) in flax.  
 A:Reference number: Z16366  
 A:Accession: T08121  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-305 <OMA>  
 A:Cross-references: UNIPROT:Q65029; EMBL:AF049681; NID:G2944416; PID:NAC05277.1; PID:925  
 A:Experimental source: cv. Stromont Cirrus  
 C:Genetics:  
 A:Gene: PER4  
 C:Superfamily: peroxidase  
 C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase  
 F:23-103/Disulfide bonds: #status predicted  
 F:50/Active site: Arg #status predicted  
 F:54-181/Binding site: heme iron (His) (axial ligands) #status predicted  
 F:56-61/Disulfide bonds: #status predicted  
 F:109-301/Disulfide bonds: #status predicted  
 F:188-213/Disulfide bonds: #status predicted

Query Match 7.0%; Score 89; DB 2; Length 305;  
 Best Local Similarity 21.9%; Pred. No. 3.9;  
 Matches 57; Conservative 39; Mismatches 92; Indels 72; Gaps 15;

QY 11 LVISASATHEAEONDSVSPKRSRVAAQNSAEVVRCLNSALQVCGCA-FACLE-NSICDTP 68  
 DB 65 ILDDTATFTGERN--AGPQNSV---RGFDIIDITKTVEACNATVSCADILALAAD 119  
 QY 69 GMYDI-----CKSFYSAKFPDQKAFVKSJLCTCIANGVSKYFLA-----110  
 DB 120 GVALVGPTTVLGRDPAITASQANAOIPAPG---SLGITITNLFTNKGLTADVTI 176  
 QY 111 -----IRCGTFORMIAEVOEECYSKLVN---CSIAKRN-PEA-----ITEVYQLP 152  
 DB 177 LSGAHTIGARCTTFRQRI-----YNDNTIDPAPATRRGNCPOGAGANLAPLDGTP 229  
 QY 153 NHSNRYNRVLV--RSLCEDEDETVST-IRDSIMEXIGPMA--SLPHILOTDHCAQ-----204  
 DB 230 TQEDNRYQDILVARRGHLHSDQELFNNGTQDALVRYTNNAAV---FATDPALANVEMG 285  
 QY 205 -----THRADFNRRRTN 217  
 DB 286 NISPLTGNTGEITFNCRKN 305

RESULT 13  
 T45954  
 hypothetical protein F708.120 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004  
 C:Accession: T45954  
 R:Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Lemk  
 Submitted to the Protein Sequence Database, January 2000  
 A:Reference number: 223018  
 A:Accession: T45954  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-473 <BEV>  
 A:Cross-references: UNIPROT:Q9LFC2; EMBL:AL137189  
 A:Experimental source: cultivar Columbia; BAC clone F708  
 C:Genetics:  
 A:Map position: 5  
 A:Intons: 29/1; 428/3  
 A:Note: F708.120  
 C:Superfamily: Arabidopsis thaliana hypothetical protein F708.130

Query Match 6.9%; Score 88; DB 2; Length 473;  
 Best Local Similarity 22.6%; Pred. No. 8.1;  
 Matches 54; Conservative 42; Mismatches 103; Indels 40; Gaps 13;

QY 27 VSPKRSVAAQNSAEVVRCLNSALQVCGCAFLEN---STCD--TDCMYDCKS-FLY 79  
 DB 16 IDEKKNVLAEGTIVLLAKRKSDPVITGILRVLYTSVDMELDDETDAKCOMLY 75



QY 80 SAAKPTQKAF-----VKESLKCIANGVTSKYFLAIRCSTFGMIAE---VOEEC-- 128  
 Db 76 PKNIRAQYRNFKNIDNTNESLKCFCG---CRFFSICRNFNSPNTSLCKGKLMNEESF 131  
 QY 129 --YSKLVNCSIAKRNPEA--ITEVQLPNHFSNRYNRLVRSLLBCDEPTVSTIRDSIME 184  
 Db 132 LEVEENDVGVPFMDSSFTITDDRLTDDST----SLLQLTKLGCADVSKLKEQYLD 187  
 QY 185 KIGPNMASIFPHILQTDHCAQTH--PPAD--FNRRRTNEPQKLVLRNLRGSEDSPSHI 239  
 Db 188 -IG-----LKEVYLMQCVFTSNTPLTDAFLKXQSNVTRKLYRKLSDKDEADPDVY 240

## RESULT 14

S45628  
 DNA-directed DNA polymerase (BC 2.7.7.7) alpha 180K chain - mouse  
 N/Alternate names: DNA polymerase alpha/DNA primase complex 180K chain  
 C/Species: Mus musculus (house mouse)  
 C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
 C/Accession: S45628; A46642  
 R:Stadlbauer, F.; Brueckner, A.; Reifues, C.; Eckerskorn, C.; Lottspeich, F.; Foerster, E.; J. Biochem. 222, 781-793, 1994  
 A>Title: DNA replication in vitro by recombinant DNA-polymerase-alpha-primase.  
 A/Reference number: S45628; PMID:94298818; PMID:8026492  
 A/Accession: S45628  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A/Residues: 1-1465 <STA>  
 A/Cross-references: UNIPROT:P33609; EMBL:D17384; NID:G937829; PIDD:BA04202.1; PID:G4424  
 R:Myazawa, H.; Izumi, M.; Tada, S.; Takada, R.; Masutani, M.; Ui, M.; Hanaoka, F.  
 J. Biol. Chem. 268, 8111-8122, 1993  
 A>Title: Molecular cloning of the cDNAs for the four subunits of mouse DNA polymerase alpha.  
 A/Reference number: A46642; PMID:93216768; PMID:8463324  
 A/Accession: A46642  
 A>Status: preliminary  
 A:Molecule type: mRNA, protein  
 A/Residues: 4-1465 <MT>  
 A/Experimental source: FM3A cells  
 A/Note: sequence extracted from NCBI backbone (NCBI:129146, NCBI:129147)  
 C/Superfamily: DNA polymerase  
 C/Keywords: DNA binding; nucleotidyltransferase; nucleus

Query Match 6.9%; Score 87.5; DB 2; Length 1465;  
 Best Local Similarity 20.7%; Pred. No. 34;  
 Matches 34; Conservative 32; Mismatches 55; Indels 43; Gaps 7;

QY 6 AVTLVIVIASAT-----HEAEONDSVSPKRPVAAQNSAEVRCUNSLAQVCGGAFA 58  
 Db 1236 AVTIALMLGLDSTQFVHQYHKOENBDAALGGPAQLTDEKTK-----DCEKFK 1284  
 QY 59 CLENSTCDTDGMWDICKSFLYSAAKPTQKAFVKESLKCIANGVT-----SKVFLAIR 112  
 Db 1285 CLCPG-CGTENIYD---NVFEGSGLDMPESLYRCGNVDCKVSPLEFWVQLSNKXLMIDR 1339  
 QY 113 RGSTPQMTAEVQEECYSKLVNCSIAKRNPEAITEVQLPNHFS 156  
 Db 1340 RCI-----KRYDGMWLC---EPTCCSRLRLPLHFS 1369

## RESULT 15

F86526  
 Mg++ transporter [imported] - Chlamydia pneumoniae (strain U138)  
 C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
 C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C/Accession: F86526  
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Shiba, T.; IS  
 Nucleic Acids Res. 28, 2311-2314, 2000  
 A>Title: Comparison of whole genome sequences of chlamydia pneumoniae U138.  
 A/Reference number: A864931; PMID:20330349; PMID:10871362  
 A/Accession: F86526  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A/Residues: 1-470 <STO>

A/Cross-references: UNIPROT:Q928Q2; GB:BA000008; NID:98978660; PIDD:BA04202.1; GSPDB:GNT  
 A/Experimental source: strain U138  
 C/Genetics:  
 A/Gene: mgtr  
 C/Superfamily: magnesium transport protein mgtr

Query Match 6.8%; Score 86; DB 2; Length 470;  
 Best Local Similarity 22.9%; Pred. No. 12;  
 Matches 47; Conservative 33; Mismatches 61; Indels 64; Gaps 13;

QY 56 AFACLENSTCDTD-GMYDICK-----SFLYSAAKPTQKAFVKESLKCIANGVTSK 106  
 Db 19 AFTCL-----STDHSDLSKIVENYNPIDLAVAVSCGPSRAILYKNLSCL-----TAK 69  
 QY 107 VFLAIR-----RCSTPQMTAEVQEECYSKLVNCSIAKRNPEAITEVQLPNHFSNRY 159  
 Db 70 VAFINTDSASRWAFIRL-----SDSEVCALEQMPPEAAVWLDIP---DRR 116  
 QY 160 YNRLVRSLLBCDEPTVSTIRDSIMEKIGPNMA-----SLPHL-----QTDHCAQTHP 207  
 Db 117 YRRLIELL---DSKALKIRD--LQKHGRNTAGRLMNEFFAFLEMTYADVACIRSNP 171  
 QY 208 RADFNRRRTNEPQKLVLRNLRGSE 232  
 Db 172 GIDLTR-----LVFVLDLFGKE 187

Search completed: November 16, 2004, 10:00:09  
 Job time : 43 secs

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OM protein - protein search, using sw model

Run on: November 16, 2004, 08:53:07 ; Search time 195 Seconds  
(without alignments)  
728,808 Million cell updates/sec

Title: US-09-703-350B-76

Perfect score: 1268

Sequence: 1 MTONSAVLLLVISASATHE.....NLRGEEDSPSIKRTSHESA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1: UniProt\_sprot:\*  
2: UniProt\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1268	100.0	247	1	STC1_HUMAN	P52823 homo sapien
2	1234	97.3	247	1	STC1_MOUSE	O55183 mus musculu
3	1231	97.1	247	1	STC1_RAT	P97574 ratu
4	1228	96.8	247	2	Q710E3	Q710E3 mus musculu
5	1228	96.8	247	2	AAC72394	AAC72394 mus muscu
6	1199	94.6	247	2	Q9N0T1	Q9N0T1 bos tauris
7	1192.5	94.0	246	2	Q7TSN9	Q7TSN9 mus musculu
8	851	67.1	253	2	Q6DF18	Q6DF18 xenopus lae
9	797	62.9	157	2	Q71UE5	Q71UE5 homo sapien
10	797	62.9	157	2	AAC87949	AAC87949 homo sapi
11	779.5	61.5	252	2	Q80014	Q80014 lepisosteus
12	778.5	61.4	252	1	Q80015	Q80015 amia calva
13	682	53.8	250	1	STC_ANGAU	P18301 anguilla au
14	662.5	52.2	256	1	STC_ONCRI	Q08264 oncorhynch
15	662.5	52.2	256	1	STC_ONCMY	P43648 oncorhynch
16	654	51.6	249	2	Q98TB7	Q98TB7 osteoglossu
17	653	51.5	249	2	Q6NVL8	Q6NVL8 brachydantio
18	653	51.5	249	2	Q6PHV3	Q6PHV3 brachydantio
19	653	51.5	249	2	AAH6540	AAH6540 brachydant
20	653	51.5	249	2	AAH65310	AAH65310 brachydant
21	617	48.7	179	1	STC_ONCKE	P43647 oncorhynch
22	354.5	28.0	296	1	STC2_MOUSE	O88452 mus musculu
23	354.5	28.0	296	2	Q9DCS6	Q9DCS6 mus musculu
24	354.5	28.0	296	2	BAB26849	BAB26849 mus muscu
25	354	27.9	302	1	STC2_HUMAN	O76061 homo sapien
26	352	27.8	302	1	STC2_MACNE	O97651 macaca neme
27	349	27.5	296	1	STC2_RAT	Q970K8 ratu
28	181.5	14.3	197	1	STC2_CAVPO	P57675 cavia porce
29	156	12.3	40	1	STC_ONCNE	P43649 oncorhynch
30	104	8.2	1044	2	Q70TF48	Q70TF48 giardia lam
31	102	8.0	473	2	Q98Z16	Q98Z16 arabidopsis

32	96.5	7.6	232	2	Q7NV12	Q7NV12 chromobacte
33	96	7.6	528	2	Q6D7B0	Q6D7B0 erwina car
34	94	7.4	1105	1	A3B1_MOUSE	Q921C1 mus musculu
35	91.5	7.2	1068	2	Q81HR6	Q81HR6 plasmodium
36	90.5	7.1	289	1	SNAA_VITVI	P93798 vitis vinif
37	90.5	7.1	454	2	Q9GV74	Q9GV74 dictyosteli
38	90.5	7.1	783	2	Q14130	Q14130 schizosacch
39	89.5	7.1	622	2	Q8H2Y0	Q8H2Y0 oryza sativ
40	89.5	7.1	3658	1	UPL2_ARATH	Q8H0T4 arabidopsis
41	89.5	7.1	9439	2	Q8CP76	Q8CP76 staphylococ
42	89	7.0	305	2	Q65029	Q65029 linum usita
43	89	7.0	996	2	Q7ZM18	Q7ZM18 brachydantio
44	89	7.0	1728	2	Q91UJ2	Q91UJ2 arabidopsis
45	88	6.9	473	2	Q9LFC2	Q9LFC2 arabidopsis

## ALIGNMENTS

RESULT 1  
STC1\_HUMAN STANDARD; PRT; 247 AA.  
AC P52823;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Stanniocalcin 1 precursor (STC-1).  
GN Name=STC1; Synonyms=STC;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fibrosarcoma, and Lung carcinoma;  
RX MEDLINE=96077825; PubMed=7489828;  
RA Chang A.C.-M., Janosi J., Hulsebeek M., de Jong D., Jeffrey K.J.,  
RA Noble J.R., Reddel R.R.;  
RT "A novel human cDNA highly homologous to the fish hormone  
RT stanniocalcin.";  
RL Mol. Cell. Endocrinol. 112:241-247(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal lung;  
RX MEDLINE=96312491; PubMed=8700837;  
RA Olsen H.S., Cepeda M.A., Zhang Q.-Q., Rosen C.A., Vozzolo B.L.,  
RA Wagner G.F.;  
RT "Human stanniocalcin: a possible hormonal regulator of mineral  
RT metabolism.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:1792-1796(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC Jeffrey K.J., Reddel R.R.;  
RT "Characterization of the human stanniocalcin 1 gene.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon, kidney, and Stomach;  
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen R.D., Schuler G.D.,  
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.R.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein W.J., Utsin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullany S.J.,  
RA Bosnak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gurratone P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [5]  
 RP SEQUENCE OF 18-32.  
 RA Zhang Z., Henzel W.,  
 RT "Signal peptide prediction based on analysis of experimentally  
 verified cleavage sites.";  
 RL Submitted (JUN-2004) to Swiss-Prot.  
 CC -1- FUNCTION: Stimulates renal phosphate reabsorption, and could  
 therefore prevent hypercalcaemia.  
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed in most tissues, with the highest  
 levels in ovary, prostate, heart, kidney and thyroid. In the  
 CC kidney, expression is confined to the nephron, specifically in the  
 CC distal convoluted tubule and in the collecting tubule. Not  
 CC detected in the brain, liver, spleen, peripheral blood leukocytes  
 CC and adrenal medulla.  
 CC -1- SIMILARITY: Belongs to the stannocalcin family.  
 CC  
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 CC  
 CC EMBL: U25997; AAC09472.1; -;  
 CC EMBL: U46768; AA88903.1; -;  
 CC EMBL: A2242179; AA179522.1; -;  
 CC EMBL: BC029044; AA829044.1; -;  
 CC Genew; HNCN;11373; STC1.  
 CC MIM: 601185; -;  
 CC GO: GO:0005179; P: hormone activity; TAS.  
 CC GO: GO:0006874; P: calcium ion homeostasis; TAS.  
 CC GO: GO:0007166; P: cell surface receptor linked signal transdu. .; TAS.  
 CC GO: GO:0007267; P: cell-cell signaling; TAS.  
 CC GO: GO:0007584; P: response to nutrients; TAS.  
 CC InterPro: IPR004978; Stannocalcin.  
 CC Pfam: PF03298; Stannocalcin; 1.  
 CC DR Direct protein sequencing; Glycoprotein; Hormone; Signal.  
 KW SIGNAL 1 17  
 FT PROPE 18 35 Potential.  
 FT CHAIN 34 247 Stannocalcin 1.  
 FT DISULFID 45 59 By similarity.  
 FT DISULFID 54 74 By similarity.  
 FT DISULFID 65 114 By similarity.  
 FT DISULFID 98 128 By similarity.  
 FT DISULFID 135 170 By similarity.  
 FT DISULFID 202 202 Interchain (By similarity).  
 FT CARBOHYD 62 62 N-linked (GlcNAc...)(Potential).  
 SQ SEQUENCE 247 AA; 27621 MW; 1E4A8BD861B49A9D CRC64;  
 Query Match 100.0%; Score 1268; DB 1; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 4-4e-102;  
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 SLEKIPNNASLFHIIQTHCQTHPRADPFRFRTRNEPKKYLRLNGEEDSPSHK 240  
 DB 181 SLEKIPNNASLFHIIQTHCQTHPRADPFRFRTRNEPKKYLRLNGEEDSPSHK 240  
 QY 241 RTSHESA 247  
 DB 241 RTSHESA 247  
 RESULT 2  
 STC1 MOUSE  
 ID STC1 MOUSE STANDARD; PRT; 247 AA.  
 AC 055183;  
 DT 15-JUL-1998 (Rel. 36, last sequence update)  
 DT 15-JUL-1998 (Rel. 36, last sequence update)  
 DT 05-JUN-2004 (Rel. 44, last annotation update)  
 DE Stannocalcin 1 precursor (STC-1).  
 GN Name=Stc1; Synonyms=Stc;  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 OK [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=97179050; PubMed=9027337;  
 RA Chang A.C.-M., Dunham M.A., Jeffrey K.J., Reddel R.R.,  
 RT "Molecular cloning and characterization of mouse stannocalcin cDNA.";  
 RL Mol. Cell. Endocrinol. 124:185-187(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Lottigiano N.A., Peters G.J., Abramson R.D., Millar S.J.,  
 RA Bosak S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.T., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Stimulates renal phosphate reabsorption, and could  
 therefore prevent hypercalcaemia (By similarity).  
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed in many tissues.  
 CC -1- SIMILARITY: Belongs to the stannocalcin family.  
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 CC  
 CC EMBL: U47815; AAC00050.1; -;  
 CC EMBL: BC021425; AA821425.1; -;  
 CC MGD; MGI:109131; Stc1.  
 CC GO: GO:0005615; C: extracellular space; IDA.  
 CC InterPro: IPR004978; Stannocalcin.

DR Pfam: PF03298; Stanniocalcin; 1.  
KM Glycoprotein; Hormone; Signal.  
FT SIGNAL 1 17 Potential.  
FT PROPEP 18 33 Stanniocalcin 1.  
FT CHAIN 34 247 By similarity.  
FT DISULFID 45 59 By similarity.  
FT DISULFID 54 74 By similarity.  
FT DISULFID 65 114 By similarity.  
FT DISULFID 98 128 By similarity.  
FT DISULFID 135 170 By similarity.  
FT DISULFID 202 202 Interchain (By similarity).  
FT CARBOHYD 62 62 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 247 AA; 27480 MW; DAD3D08575A513B CRC64;  
Query Match 97.3%; Score 1234; DB 1; Length 247;  
Best Local Similarity 96.4%; Pred. No. 4e-99; Indels 0; Gaps 0;  
Matches 238; Conservative 5; Mismatches 4;  
QY 1 MLQNSAVLIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVGGAFAC 60  
DB 1 MLQNSAVLIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVGGAFAC 60  
QY 61 ENSTCDTGMWDICKSFYSAKFDTOGKAFVKSILKCIANGVTSKVFALIRCGSTFOR 120  
DB 61 ENSTCDTGMWDICKSFYSAKFDTOGKAFVKSILKCIANGVTSKVFALIRCGSTFOR 120  
QY 121 IAEVQECYSKLVNCSIAKRNPEALTEVQJPNHFSNRYNRLVRSLLCEDEDTYSTIRD 180  
DB 121 IAEVQECYSKLVNCSIAKRNPEALTEVQJPNHFSNRYNRLVRSLLCEDEDTYSTIRD 180  
QY 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRTRNEPQKLKVLRLNGEEDSPSHIK 240  
DB 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRTRNEPQKLKVLRLNGEEDSPSHIK 240  
QY 241 RTSHESA 247  
DB 241 RTSHESA 247  
RESULT 3  
STCL\_RAT STANDARD; PRT: 247 AA.  
ID STCL\_RAT STANDARD; PRT: 247 AA.  
AC P97574;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Stanniocalcin 1 precursor (STC-1).  
GN Name=Stc1; Synonyms=Stc;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;  
RA Aoe T., Yamamoto M., Hall A.E., Brown E.M., Hebert S.C.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Stimulates renal phosphate reabsorption, and could  
CC therefore prevent hypercalcaemia (By similarity).  
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the stanniocalcin family.  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
DR EMBL: U62667; AAC39541.1; -  
DR RGD: 621776; Stcl.

DR InterPro: IPR004978; Stanniocalcin.  
KM Glycoprotein; Hormone; Signal.  
FT SIGNAL 1 17 Potential.  
FT PROPEP 18 33 Stanniocalcin 1.  
FT CHAIN 34 247 By similarity.  
FT DISULFID 45 59 By similarity.  
FT DISULFID 54 74 By similarity.  
FT DISULFID 65 114 By similarity.  
FT DISULFID 98 128 By similarity.  
FT DISULFID 135 170 By similarity.  
FT DISULFID 202 202 Interchain (By similarity).  
FT CARBOHYD 62 62 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 247 AA; 27507 MW; DAC2FD08575A513B CRC64;  
Query Match 97.1%; Score 1231; DB 1; Length 247;  
Best Local Similarity 96.0%; Pred. No. 7.3e-99; Indels 0; Gaps 0;  
Matches 237; Conservative 6; Mismatches 4;  
QY 1 MLQNSAVLIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVGGAFAC 60  
DB 1 MLQNSAVLIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVGGAFAC 60  
QY 61 ENSTCDTGMWDICKSFYSAKFDTOGKAFVKSILKCIANGVTSKVFALIRCGSTFOR 120  
DB 61 ENSTCDTGMWDICKSFYSAKFDTOGKAFVKSILKCIANGVTSKVFALIRCGSTFOR 120  
QY 121 IAEVQECYSKLVNCSIAKRNPEALTEVQJPNHFSNRYNRLVRSLLCEDEDTYSTIRD 180  
DB 121 IAEVQECYSKLVNCSIAKRNPEALTEVQJPNHFSNRYNRLVRSLLCEDEDTYSTIRD 180  
QY 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRTRNEPQKLKVLRLNGEEDSPSHIK 240  
DB 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRTRNEPQKLKVLRLNGEEDSPSHIK 240  
QY 241 RTSHESA 247  
DB 241 RTSHESA 247  
RESULT 4  
Q71UE3 PRELIMINARY; PRT: 247 AA.  
ID Q71UE3 PRELIMINARY; PRT: 247 AA.  
AC Q71UE3;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Stanniocalcin.  
GN Mus musculus (Mouse).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC Varghese R., Wong C.K.C., Doel H., Wagner G.F., Dimattia G.E.;  
RT "Comparative Analysis of Mammalian Stanniocalcin Genes";  
RL Endocrinology 139:4717-4725(1998).  
DR EMBL: AF099098; AAC72394.1; -  
DR GO: GO:0005615; C:extracellular space; IDA.  
DR InterPro: IPR000719; Prot kinase.  
DR InterPro: IPR004978; Stanniocalcin.  
DR Pfam: PF03298; Stanniocalcin; 1.  
DR PROSITE: PS00107; PROTEIN KINASE ATP; UNKNOWN 1.  
SQ SEQUENCE 247 AA; 27495 MW; CAZDEDE659BAACB CRC64;  
Query Match 96.8%; Score 1228; DB 2; Length 247;  
Best Local Similarity 96.0%; Pred. No. 1.3e-98; Indels 0; Gaps 0;  
Matches 237; Conservative 5; Mismatches 5;  
QY 1 MLQNSAVLIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVGGAFAC 60  
DB 1 MLQNSAVLIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVGGAFAC 60

[illegible]

RESULT	5
AAC72394	
AACT2394	PRELIMINARY; PRT; 247 AA.
ID AAC72394	
AC AAC72394	
DT 02-MAR-2004 (TREMBLrel. 27, Created)	
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)	
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)	
DS Stannocalcin precursor.	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	
OC NCBI_FaxID=10090;	
XX [1]	
RN	SEQUENCE FROM N.A.
RP	
RA Varghese R., Wong C.K.C., Doel H., Wagner G.F., DiMatteo G.B.,	
RT "Comparative Analysis of Mammalian Stannocalcin Genes";	
RL Endocrinology 139:4717-4725 (1998).	
DR EMBL, AF039098; AAC72394.1	
SO SEQUENCE 247 AA; 27495 MW; CA2DEB559EAAFCB CRC64;	

Query Match	96.8%;	Score 1228;	DB 2;	Length 247;
Best Local Similarity	96.0%;	Pred. No. 1.3e-98;		
Matches 237; Conservative	5;	Mismatches	5;	Indels 0; Gaps 0

QY	MLONSAYLLVLYVTSASATHEAEONSVSPRKRRVAQNSAEVYRCUNSLALOVGGAAFL	60
Db	1 MLONSAYLLVLYVTSASAAHEAEONDSVSPRKRRVAQNSAEVYRCUNSLALOVGGAAFL	60
QY	61 ENSTCTDGMAYDCKSFVLSAAKPTDQKAFYKESLKTANGVTSKYFLAIRCSTFQRM	120
Db	61 ENSTCTDGMAYDCKSFVLSAAKPTDQKAFYKESLKTANGVTSKYFLAIRCSTFQRM	120
QY	121 IAAVEQECYSKLVNCSIAKRNPEALTVEYVQLPNHSNRYRLVRSLLCEDEPTVSTRD	180
Db	121 IAAVEQECYSKLVNCSIAKRNPEALTVEYVQLPNHSNRYRLVRSLLCEDEPTVSTRD	180
QY	181 SLMEKIGPNMASLFIHLQTDHCQAQTHPRADFNRRTNPEOKLYLLNLRGEEDSPSHIK	240
Db	181 SLMEKIGPNMASLFIHLQTDHCQAQTHPRADFNRRTNPEOKLYLLNLRGEEDSPSHIK	240
QY	241 RTSHESA 247	
Db	241 RTSQESA 247	

RESULT 6		
ID	Q9NOT1	PRT: 247 AA.
AC	Q9NOT1	PRELIMINARY;
DT	01-OCT-2000 (TREMBL) 15, Last seq	
DT	01-OCT-2000 (TREMBL) 15, Last seq	
DT	01-MAR-2004 (TREMBL) 26, Last seq	
DE	Scatolocalin.	
OS	Bos taurus (Bovine).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Amniota; Mammalia; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	
OC	Memellata; Euteria;	

OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
[]  
RP SEQUENCE FROM N.A.  
RN  
RC TISSUE=Ovary;  
RA DiMattea G.E.;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases  
DR EMBL; AF257506; AA68896.1; -  
DR GO; GO:0005576; Cytochrome11a1a; IEA.  
DR GO; GO:0005179; F11homone activity; IEA.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR004978; Stannocalcain.  
DR Pfam; PF03288; Stannocalcain; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN 1.  
SQ SEQUENCE 247 AA; 2755 MW; F9942A715E2A3D80 CRC64;

Query Match	94.6%;	Score 1199;	DB 2;	Length 247;
Best Local Similarity	94.7%;	Pred. No. 4.4e-96;		
Matches 234;	Conservative 5;	Mismatches 8;	Indels 0;	Gaps 0;

QY	MLNSAVILVIVISASATHEAEQNDVS6PRKSRVAAQMSAEVHCLMSALQVGGAGACL	60
Db	1 MLQNSAVILVIVISASATHEAEQNDVS6LRKSRVAAQMSAEVHCLMSALQVGGAGACL	60
QY	ENSTCTDQGYDI CKSFLYSAAKPTQGA FYKESLCTIANGVTSTKFLAIRRSTFORM	120
Db	61 ENSTCTDQGYDI CKSFLYSAAKPTQGA FYKESLCTIANGVTSTKFLAIRRSTFORM	120
QY	IAEVOECYSKLVNCSIAKRNPEALTTEVVOJPNHFSNRYYRVLVRSLLCEDEPTVSIRI	180
Db	121 IAEVOECYSKLVNCSIAKRNPEALTTEVVOJPNHFSNRYYRVLVRSLLCEDEPTVSIRI	180
QY	SLMEKIGPNNMASIFHILQTDHCAQTHPRADFNRRRTNEPOXLKVLLENLRGEEDSPSHIK	240
Db	181 SLMEKIGPNNMASIFHILQTDHCAQTHPRADFNRRRTNEPOXLKVLLENLRGEEDSPSHIK	240
QY	RTSHESA 247	
Db	241 RTSHESA 247	
Db	241 RTQGBSA 247	

RESULT	7
QOTSNS9	PRELIMINARY; PRI; 246 AA.
ID QOTSNS9	
AC QOTSNS9	
DT 01-OCT-2003 (Tremblrel. 25, Created)	
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)	
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)	
DE Stanniocalcin 1.	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	
OX NCBI_TaxID=10090;	
XP [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=129/SvJ	
RA Chang A.C., Cha J., Reddel R.R.;	
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.	
RL EMBL; AF512563; AAP47156.1; -	
DR GO; GO:0005576; Cytosolic activity; IEA.	
DR GO; GO:0005179; F-actinome activity; IEA.	
DR InterPro; IPR004978; Stanniocalcin.	
DR Pfam; PF03288; Stanniocalcin; 1.	
QO SEQUENCE 246 AA; 27423 MW; 4101C37BB6D743B2 CRC64;	

Query Match	94.0%;	Score 1192.5;	DB 2;	Length 246;
Best Local Similarity	93.9%;	Pred. No. 1.6e-95;		
Matches 232;	Conservative 7;	Mismatches 7;	Indels 1;	Gaps 1;

Qy 1 M L Q S A V L L V I S A S A T H E A Q N D S V P K R S V A A Q S A E V V R C L N S L Q V G C C A F A C L 600  
| | | | | : | | | | | | | | | | | | | | | : : | | | |  
Db 1 M L Q S A V I L L V I S A A A H E A Q N D S V P K R S V A A Q S A E V V R C L N S A C R L A A G - F A C L 599

QY 61 ENSTCCTDGMVDICSFYSAKFPDQGAFFYKESIKCIANGVTSKVFALIRCGSTFORM 120  
DB 60 ENSTCCTDGMVDICSFYSAKFPDQGAFFYKESIKCIANGVTSKVFALIRCGSTFORM 119  
QY 121 IAEVQECYSKLVNCSIAKRNPEALTEVQLPNHFSENRYNRLVLSLEDCDEDTVSTIR 180  
DB 120 IAEVQDCYSKLVNCSIAKRNPEALTEVQLPNHFSENRYNRLVLSLEDCDEDTVSTIR 179  
QY 181 SLMEKIGPNWASIFHILQTDHCQOTHPRADFNRRRNPEPOKLVILRNLRGSDPSHIK 240  
DB 180 SLMEKIGPNWASIFHILQTDHCQOTHPRADFNRRRNPEPOKLVILRNLRGSDPSHIK 239  
QY 241 RTSSEA 247  
DB 240 RTSSEA 246

## RESULT 8

Q6DF18 PRELIMINARY; PRT; 253 AA.

AC Q6DF18  
DT 01-OCT-2004 (TRENBLrel. 28, Created)  
DT 01-OCT-2004 (TRENBLrel. 28, Last sequence update)  
DT 01-OCT-2004 (TRENBLrel. 28, Last annotation update)  
DE Hypothetical protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
OC Xenopodidae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Pearce C.,  
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Millar J.S.,  
RA Bosak S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.V., Huylk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalins D.E., Schmech A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RL [2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Kidney;  
RC MEDLINE=22341132; PubMed=12454917;  
RA Klein S.L., Strausberg R., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT Initiative";  
RT Dev. Dyn. 225:384-391(2002).  
RL [3]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Kidney;  
RC Klein S., Strausberg R.;  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
KW EMBL: BC076749; AA076749.1; -  
SQ Hypothetical protein. 253 AA; 28127 MW; DFC93366DA31765D CRC64;

Query Match 67.1%; Score 851; DB 2; Length 253;

Best Local Similarity 69.6%; Pred. No. 8.5e-66;  
Matches 160; Conservative 37; Mismatches 31; Indels 2; Gaps 2;  
QY 8 LVLVVISATHEAEQNDVS-SPRKS-RVAQNSAEVYRCINSLAQVCGCAFLENSTC 65  
DB 12 LLLNVSCTGSDSDPNDPSQGIKRGIRLASQISEVAVRCINGALQVCGCAFLENSTC 71  
QY 66 DTDCGMVDICSFYSAKFPDQGAFFYKESIKCIANGVTSKVFALIRCGSTFORMIAEVQ 125  
DB 72 DTDCGMVDICSFYSAKFPDQGAFFYKESIKCIANGVTSKVFALIRCGSTFORMIAEVQ 131  
QY 126 EECYSKLVNCSIAKRNPEALTEVQLPNHFSENRYNRLVLSLEDCDEDTVSTIRDSIMEX 185  
DB 132 QDCYTKMDICTVAQNPDAITEVHLPQHFSENRYNRLVLSLEDCDEDTVSAVKSIMEQ 191  
QY 186 IGPWNASIFHILQTDHCQOTHPRADFNRRRNPEPOKLVILRNLRGSDPS 235  
DB 192 IGPWNASIFHILQTDHCQOTHPRADFNRRRNPEPOKLVILRNLRGSDPS 241

## RESULT 9

Q71UES PRELIMINARY; PRT; 157 AA.

AC Q71UES  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
DE Stanniocalcin (Fragment).  
GN Name=STC;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99008615; PubMed=9794484;  
RA Varghese R., Wong C.K., Deol H., Wagner G.F., DiMatteo G.E.;  
RT "Comparative analysis of mammalian stanniocalcin genes";  
RL Endocrinology 139:4714-4725(1998).  
DR EMBL: AF098463; AAC97949.1; -  
DR InterPro: IPR000719; Prot. Kinase.  
DR InterPro: IPR004978; Stanniocalcin.  
DR Pfam: PF00298; Stanniocalcin.1  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
FT NON\_TER 157  
SQ SEQUENCE 157 AA; 17094 MW; E22F2A6067966C3E CRC64;

Query Match 62.9%; Score 797; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 2.4e-61;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLVVISATHEAEQNDVS-SPRKSRYVAQNSAEVYRCINSLAQVCGCAFACL 60  
DB 1 MLQNSAVLVVISATHEAEQNDVS-SPRKSRYVAQNSAEVYRCINSLAQVCGCAFACL 60  
QY 61 ENSTCCTDGMVDICSFYSAKFPDQGAFFYKESIKCIANGVTSKVFALIRCGSTFORM 120  
DB 61 ENSTCCTDGMVDICSFYSAKFPDQGAFFYKESIKCIANGVTSKVFALIRCGSTFORM 120  
QY 121 IAEVQECYSKLVNCSIAKRNPEALTEVQLPNHFSEN 157  
DB 121 IAEVQECYSKLVNCSIAKRNPEALTEVQLPNHFSEN 157

## RESULT 10

AAC97949 PRELIMINARY; PRT; 157 AA.

AC AAC97949  
DT 02-MAR-2004 (TRENBLrel. 27, Created)  
DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)  
DE Stanniocalcin (Fragment).  
GN STC.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99008615; PubMed=9794484;  
 RA Varghese R., Wong C.K., Deol H., Wagner G.F., Dimattia G.E.;  
 RT "Comparative analysis of mammalian stanniocalcin genes.";  
 RL Endocrinology 139:4714-4725(1998).  
 DR EMBL, AF098463; AAC97949.1; -.  
 FT NON\_TER  
 SQ SEQUENCE 157 AA; 17094 MW; E22F2A6067966C3E CRC64;

Query Match 62.9%; Score 797; DB 2; Length 157;  
 Best Local Similarity 100.0%; Pred. No. 2, 4e-61;  
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLTASATHEAEONDSVSPKRSVVAQNSAEVRCINSALQVCGCAFACL 60  
 DB 1 MLQNSAVLLVLTASATHEAEONDSVSPKRSVVAQNSAEVRCINSALQVCGCAFACL 60  
 QY 61 ENSTCTDGMWDICKSFVSAKFDTGKAFVKESIKCIANGVTSKVFLAIRCSTFORM 120  
 DB 61 ENSTCTDGMWDICKSFVSAKFDTGKAFVKESIKCIANGVTSKVFLAIRCSTFORM 120  
 QY 121 IAEVQECYSKLVNCSIAKRNPEAITREVQLPNHFSN 157  
 DB 121 IAEVQECYSKLVNCSIAKRNPEAITREVQLPNHFSN 157

## RESULT 11

Q80014 PRELIMINARY; PRT; 252 AA.  
 AC Q80014;  
 DT 01-JUN-2003 (TRENBLREL. 24, Created)  
 DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)  
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)  
 DE Stanniocalcin precursor.  
 GN Name=Stc;  
 OS Lepisosteus osseus (long-nosed gar).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;  
 OC Lepisosteus  
 CX NCBI\_TaxID=34771;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=14697312;  
 RA Amemiya Y., Youson J.H.;  
 RT "Primary structure of stanniocalcin in two basal Actinopterygii.";  
 RL Gen. Comp. Endocrinol. 135:250-257(2004).  
 DR EMBL, AB106623; BAC66164.1; -.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005179; F:hormone activity; IEA.  
 DR InterPro; IPR000719; P:prot\_kinase.  
 DR InterPro; IPR004978; Stanniocalcin.  
 DR Pfam; PF03298; Stanniocalcin; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
 KW Signal.  
 FT SIGNAL 1 32 Potential.  
 FT CHAIN 33 252 Potential.  
 SQ SEQUENCE 252 AA; 27936 MW; 2C99E88DCCED2E33 CRC64;

Query Match 61.5%; Score 779.5; DB 2; Length 252;  
 Best Local Similarity 59.8%; Pred. No. 1, 4e-59;  
 Matches 152; Conservative 44; Mismatches 49; Indels 9; Gaps 3;

QY 1 MLQNSAVLLVLTASATHEAEONDSVSPKRSVVAQNSAEVRCINSALQVCGCAFACL 60  
 DB 1 MLQNSAVLLVLTASATHEAEONDSVSPKRSVVAQNSAEVRCINSALQVCGCAFACL 59  
 QY 61 ENSTCTDGMWDICKSFVSAKFDTGKAFVKESIKCIANGVTSKVFLAIRCSTFORM 120  
 DB 61 ENSTCTDGMWDICKSFVSAKFDTGKAFVKESIKCIANGVTSKVFLAIRCSTFORM 120

DB 60 ENSTCTDGMWDICKSFVSAKFDTGKAFVKESIKCIANGVTSKVFLAIRCSTFORM 119  
 QY 121 IAEVQECYSKLVNCSIAKRNPEAITREVQLPNHFSNRYNRLVRLSCDEDEVTIR 180  
 DB 120 IAEVQECYSKLVNCSIAKRNPEAITREVQLPNHFSNRYNRLVRLSCDEDEVTIR 179  
 QY 181 SLMEKIGPNNASLPHILQDHCACOTHPRAD-----FNRRTNEPKLKVLLRNLRGEE 233  
 DB 180 SLVRLGPNAMLQLQSKRCPSSSSLSPPAGAEGRGNRWPIGPVFR-MQDNLRREP 238  
 QY 234 DSPSHIKRTSHESA 247  
 DB 239 SLFSPKRSADSS 252

## RESULT 12

Q80015 PRELIMINARY; PRT; 252 AA.  
 AC Q80015;  
 DT 01-JUN-2003 (TRENBLREL. 24, Created)  
 DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)  
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)  
 DE Stanniocalcin precursor.  
 GN Name=Stc;  
 OS Amlia calva (Bowfin).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Amiiformes; Amliidae; Amlia.  
 CX NCBI\_TaxID=7924;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=14697312;  
 RA Amemiya Y., Youson J.H.;  
 RT "Primary structure of stanniocalcin in two basal Actinopterygii.";  
 RL Gen. Comp. Endocrinol. 135:250-257(2004).  
 DR EMBL, AB106622; BAC66163.1; -.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005179; F:hormone activity; IEA.  
 DR InterPro; IPR000719; P:prot\_kinase.  
 DR InterPro; IPR004978; Stanniocalcin.  
 DR Pfam; PF03298; Stanniocalcin; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
 KW Signal.  
 FT SIGNAL 1 32 Potential.  
 FT CHAIN 33 252 Potential.  
 SQ SEQUENCE 252 AA; 27868 MW; B9D9663610DF0B5D CRC64;

Query Match 61.4%; Score 778.5; DB 2; Length 252;  
 Best Local Similarity 69.8%; Pred. No. 1, 7e-59;  
 Matches 141; Conservative 37; Mismatches 23; Indels 1; Gaps 1;

QY 1 MLQNSAVLLVLTASATHEAEONDSVSPKRSVVAQNSAEVRCINSALQVCGCAFACL 60  
 DB 1 MLQNSAVLLVLTASATHEAEONDSVSPKRSVVAQNSAEVRCINSALQVCGCAFACL 59  
 QY 61 ENSTCTDGMWDICKSFVSAKFDTGKAFVKESIKCIANGVTSKVFLAIRCSTFORM 120  
 DB 60 ENSTCTDGMWDICKSFVSAKFDTGKAFVKESIKCIANGVTSKVFLAIRCSTFORM 119  
 QY 121 IAEVQECYSKLVNCSIAKRNPEAITREVQLPNHFSNRYNRLVRLSCDEDEVTIR 180  
 DB 120 IAEVQECYSKLVNCSIAKRNPEAITREVQLPNHFSNRYNRLVRLSCDEDEVTIR 179  
 QY 181 SLMEKIGPNNASLPHILQDHC 202  
 DB 180 NIVSRGPNMSMLFQLQSKPC 201

RESULT 13  
 ID STC ANGAU STANDARD; PRT; 250 AA.  
 AC P18301;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)



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DE 05-Jun-2004 (Rel. 44, Last annotation update)
DE Stannocalcin precursor (STC) (Coproporphyrinogen desaminase) (CS)
DE (Hypocalcin) (Teleocalcin).
GN Name=STC;
OS Anguilla australis (Australian eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=7940;
RN
RP SEQUENCE FROM N.A., AND SEQUENCE OF 33-57.
RX MEDLINE=88083961; PubMed=3319739;
RA Butkus A., Roche P.J., Fernley R.T., Haralambidis J., Penshaw J.D.,
RA Ryan G.B., Trahair J.F., Tregear G.W., Coghlan J.P.;
RT "Purification and cloning of a cDNAs of Stannus protein from
RT Anguilla australis";
RL Mol. Cell. Endocrinol. 54:123-133(1987).
RN
RP REVISIONS.
RA Roche P.J.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC
CC -!- FUNCTION: Its primary function is the prevention of hypercalcemia.
CC Upon release into the circulation, it lowers calcium transport by
CC the gills, thereby reducing its rate of influx from the
CC environment into the extracellular compartment. STC also
CC stimulates phosphate reabsorption by renal proximal tubules. The
CC consequence of this action is increased levels of plasma
CC phosphate, which combines with excess calcium and promotes its
CC disposal into bone and scales.
CC -!- SUBUNIT: Homodimer, disulfide-linked.
CC -!- TISSUE SPECIFICITY: Corpuseles of Stannus.
CC -!- SIMILARITY: Belongs to the stannocalcin family.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
CC The European Bioinformatics Institute. There are no restrictions on
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sdb.ch/announce
CC or send an email to license@isb-sdb.ch).
CC
CC -----
DR EMBL; M36967; AAB91483.1; -.
DR PIR; A54648; A54648.
DR InterPro; IPR004978; Stannocalcin.
DR Pfam; PF03298; Stannocalcin; 1.
KW Direct protein sequencing; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 17 Potential.
FT PROPEP 18 32 Potential.
FT CHAIN 33 250 Stannocalcin.
FT DISULFID 44 58 By similarity.
FT DISULFID 53 73 By similarity.
FT DISULFID 64 113 By similarity.
FT DISULFID 97 127 By similarity.
FT DISULFID 134 169 By similarity.
FT DISULFID 201 201 Interchain (By similarity).
FT CARBOHYD 61 61 N-linked (GlcNAc...) (Probable).
SQ
SEQUENCE 250 AA; 27174 MW; BB972BD951F75B3E CRC64;

Query Match 53.8%; Score 682; DB 1; Length 250;
Best Local Similarity 54.3%; Pred. 4.2e-51;
Matches 138; Conservative 47; Mismatches 57; Indels 12; Gaps 6

QY 1 MTONSAVLLVLTYSATHEAQNQSVSPRKSRVAQNAEYVRGCAINSALQVGCAGFACL 60
DB 1 MNRSGLLITLVA-VTAAYEQDESEPLSRTPAFSASSSDVARCLNGALQVGCASFACL 59
QY 61 ENSTCDTDMQYDICKSFLVSAKFTDQGFAYKESLKIANGVTSKVFIAIRPCSTFORM 120
DB 60 DSTNCITDMHEICRSFLHGAAKFTDQGTFTVYESIKCIANGITTSKVFTIIRCSSTFORM 119
QY 121 IAEVDECKSKINVCISIAKRNPEALTEVQOLPMHFSNRYYNLMRSLGDCDEDTYSITRD 160
DB 120 ISEVDECKSKIDLVQASQNPBAQGEVQVQSPFNRRYITSLQSLTCDDEDTYEQVRA 179

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Qy	18	SLMEKIPPMNA5LPHIIQITDHC-----AQTHP-RADFNRRRTNPQKTLVLRNGEED	234
Db	180	GLVRLRPENGVLFQIIQITKACPSAAGCTGCPVAGGSKWRPMKPMPEFKI-QPHLRSD	237
Qy	235	SPSHI--KRTSHES	246
Db	238	-PTHLPKKRSTSS	250
RESULT 14			
STC_ONCKI	STC_ONCKI	STANDARD;	PRF; 256 AA.
AC	Q08264;		
DT	01-FEB-1995 (Rel. 31, Created)		
DT	01-FEB-1995 (Rel. 31, Last sequence update)		
DT	05-JUN-2004 (Rel. 44, Last annotation update)		
DE	Stanniocalcin precursor (STC) (Carpuscles of Stannius protein) (CS)		
DE	(Hypocalcin) (Teleocalcin).		
GN	Name=STC;		
OS	Oncorhynchus kisutch (Coho salmon);		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;		
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.		
OX	NCBI_TaxID=8019;		
RL	[1]		
RP	SEQUENCE FROM N.A.		
FX	MEDLINE=93246046; PubMed=1363790;		
RA	Wagner G.F., Dinattuta G.E., Davie J.R., Copp D.H., Friesen H.G.;		
RT	"Molecular cloning and cDNA sequence analysis of coho salmon		
RT	stanniocalcin";		
RL	Mol. Cell. Endocrinol. 90:7-15 (1992).		
RN	[2]		
RP	SEQUENCE OF 34-73.		
FX	MEDLINE=89065334; PubMed=3197944;		
RA	Wagner G.F., Fernick J.C., Park C.M., Milliken C., Copp D.H.,		
RA	Friesen H.G.;		
RT	"Comparative biochemistry and physiology of teleocalcin from sockeye		
RT	and coho salmon.";		
RL	Gen. Comp. Endocrinol. 72:237-246 (1988).		
CC	-I- FUNCTION: Its primary function is the prevention of hypercalcemia.		
CC	upon release into the circulation, it lowers calcium transport by		
CC	the gills, thereby reducing its rate of influx from the		
CC	environment into the extracellular compartment. STC also		
CC	stimulates phosphate reabsorption by renal proximal tubules. The		
CC	consequence of this action is increased levels of plasma		
CC	phosphate, which combines with excess calcium and promotes its		
CC	disposal into bone and scales.		
CC	-I- SUBUNIT: Homodimer; disulfide-linked.		
CC	-I- SUBCELLULAR LOCATION: Secreted.		
CC	-I- TISSUE SPECIFICITY: Produced and secreted by the corpuscles of		
CC	Stannius.		
CC	-I- SIMILARITY: Belongs to the stanniocalcin family.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation		
CC	at the European Bioinformatics Institute. There are no restrictions on		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
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CC	or send an email to <a href="mailto:license@isb-sdb.ch">license@isb-sdb.ch</a> ).		
CC	-----		
DR	EMBL; S59519; AAB26419.1; -.		
DR	PIR; B60841; B60841.		
DR	PIR; I51197; I51197.		
DR	InterPro; IPR004978; Stanniocalcin.		
DR	Pfam; PF032981; Stanniocalcin; 1.		
KW	Calcium transport; Direct protein sequencing; Glycoprotein; Hormone;		
KW	Signal.		
FT	SIGNAL	1	18 Potential.
FT	PROPEP	19	33 By similarity.
FT	CHAIN	34	256 Stanniocalcin.
FT	CARBOHYD	62	62 N-linked (GlcNAc . . .).

SQ SEQUENCE 256 AA; 28074 MW; E688B930B394A8D3 CRC64;  
 Query Match 52.2%; Score 662.5; DB 1; Length 256;  
 Best Local Similarity 53.4%; Pred. No. 2,2e-49;  
 Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;  
 QY 11 LVISASATHEAQNDSVSPKRSVVAQNSAEVVRCLNSALQVCGGAFACLENSTCDTDGM 70  
 12 LVIGTAAFTDPTDEBA-SPRRARFSSNSPSDVARCINGALAVCGCFACLENSTCDTDGM 70  
 QY 71 YDIKSFVSAKPDVQKAFVKESELKCIANGVTSKVFLAIRCSTFORMIAVEQECYS 130  
 71 HDICQLFFHTAATFNTQKTFVKESELKCIANGVTSKVFLAIRCSTFORMIAVEQECYS 130  
 Db 71 HDICQLFFHTAATFNTQKTFVKESELKCIANGVTSKVFLAIRCSTFORMIAVEQECYS 130  
 QY 131 KLVNCSIAKRNPEATEVVOLEPNHFSNRYNRLVRSLLCEDETVSTIRDSIMEKIGPM 190  
 131 RLDICGVARSNPEAIGEVVQVPAHFNRRYSTLLQSLACDEBTVAVVAAGIARLGPDM 190  
 Db 131 RLDICGVARSNPEAIGEVVQVPAHFNRRYSTLLQSLACDEBTVAVVAAGIARLGPDM 190  
 QY 191 ASLFIHLQTDHCAQTHPRADF-----RRRTNPEQTLKYLRLRGEESPSHI 239  
 191 ETLFOLLQNHCHQPSGNSQGNPSAPAGRWPMGSPPSFKI-QPSMRGRD--PTH 241  
 Db 191 ETLFOLLQNHCHQPSGNSQGNPSAPAGRWPMGSPPSFKI-QPSMRGRD--PTH 241  
 RESULT 15  
 STC ONCMY STANDARD; PRT; 256 AA.  
 ID STC ONCMY STANDARD; PRT; 256 AA.  
 AC P43648; Q98SE1;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Stanniocalcin precursor (STC) (Corpuscles of Stannius protein) (CS)  
 DE (Hypocalcin) (Teleocalcin).  
 GN Name:STC;  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RA McCudden C.R.; Wagner G.F.;  
 RT "Rainbow trout ovarian stanniocalcin";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 34-66.  
 RC TISSUE=Stannius corpuscles;  
 RA MEDLINE=88196801; PubMed=3360288;  
 RA Lafeber F.P.J.G.; Hansen R.G.J.M.; Choy Y.M.; Flik G.;  
 RA Hermann-Erlée M.P.M.; Pang P.K.T.; Wendelaar Bonga S.E.;  
 RT "Identification of hypocalcin (teleocalcin) isolated from trout  
 Stannius corpuscles";  
 RL Gen. Comp. Endocrinol. 69:19-30(1998).  
 CC -1- FUNCTION: Its primary function is the prevention of hypercalcemia.  
 CC Upon release into the circulation, it lowers calcium transport by  
 CC the gills, thereby reducing its rate of influx from the  
 CC environment into the extracellular compartment. STC also  
 CC stimulates phosphate reabsorption by renal proximal tubules. The  
 CC consequence of this action is increased levels of plasma  
 CC phosphate, which combines with excess calcium and promotes its  
 CC disposal into bone and scales.  
 CC -1- SUBUNIT: Homodimer; disulfide-linked.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Produced and secreted by the corpuscles of  
 CC Stannius.  
 CC -1- SIMILARITY: Belongs to the stanniocalcin family.  
 CC  
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 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
 CC -----  
 CC EMBL: AF326317; AK01423.1; -  
 CC DR EMBL: AF326318; AK01424.1; -  
 CC DR InterPro: IPR004978; Stanniocalcin.  
 CC DR Pfam: PF03298; Stanniocalcin; 1.  
 CC KW Calcium transport; Direct protein sequencing; Glycoprotein; Hormone;  
 CC Signal.  
 CC FT SIGNAL. 1 18 Potential.  
 CC FT PROPEP 19 33  
 CC FT CHAIN 34 256 Stanniocalcin.  
 CC FT CARBOHYD 62 62 N-linked (GlcNAc...).  
 CC FT VARIANT 41 41 D -> E.  
 CC SQ SEQUENCE 256 AA; 28104 MW; E688A0E0B394A8D3 CRC64;  
 Query Match 52.2%; Score 662.5; DB 1; Length 256;  
 Best Local Similarity 53.4%; Pred. No. 2,2e-49;  
 Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;  
 QY 11 LVISASATHEAQNDSVSPKRSVVAQNSAEVVRCLNSALQVCGGAFACLENSTCDTDGM 70  
 12 LVIGTAAFTDPTDEBA-SPRRARFSSNSPSDVARCINGALAVCGCFACLENSTCDTDGM 70  
 Db 12 LVIGTAAFTDPTDEBA-SPRRARFSSNSPSDVARCINGALAVCGCFACLENSTCDTDGM 70  
 QY 71 YDIKSFVSAKPDVQKAFVKESELKCIANGVTSKVFLAIRCSTFORMIAVEQECYS 130  
 71 HDICQLFFHTAATFNTQKTFVKESELKCIANGVTSKVFLAIRCSTFORMIAVEQECYS 130  
 Db 71 HDICQLFFHTAATFNTQKTFVKESELKCIANGVTSKVFLAIRCSTFORMIAVEQECYS 130  
 QY 131 KLVNCSIAKRNPEATEVVOLEPNHFSNRYNRLVRSLLCEDETVSTIRDSIMEKIGPM 190  
 131 RLDICGVARSNPEAIGEVVQVPAHFNRRYSTLLQSLACDEBTVAVVAAGIARLGPDM 190  
 Db 131 RLDICGVARSNPEAIGEVVQVPAHFNRRYSTLLQSLACDEBTVAVVAAGIARLGPDM 190  
 QY 191 ASLFIHLQTDHCAQTHPRADF-----RRRTNPEQTLKYLRLRGEESPSHI 239  
 191 ETLFOLLQNHCHQPSGNSQGNPSAPAGRWPMGSPPSFKI-QPSMRGRD--PTH 241  
 Db 191 ETLFOLLQNHCHQPSGNSQGNPSAPAGRWPMGSPPSFKI-QPSMRGRD--PTH 241

Search completed: November 16, 2004, 09:59:23  
 Job time : 197 secs



Query Match 100.0%; Score 1268; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9.3e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MLQNSAVLLVIVISASATHEAEQNDVSVPKRSVVAQNSAEVVRCLNSALQVCGAFACL 60
DB 1 MLQNSAVLLVIVISASATHEAEQNDVSVPKRSVVAQNSAEVVRCLNSALQVCGAFACL 60
QY 61 ENSTCDTDGMYDICKSFLYSAKFDTOGKAFVKSILKCIANGVTSKYFLAIRRCSFTQRM 120
DB 61 ENSTCDTDGMYDICKSFLYSAKFDTOGKAFVKSILKCIANGVTSKYFLAIRRCSFTQRM 120
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHSNRYNRLVRSLLCEDDVTSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHSNRYNRLVRSLLCEDDVTSTIRD 180
QY 181 SLMEKIGPNVASLPHILQTDHCQOTHPRADPNRRRTNEPOKLVLLRNLRGGEEDSPSHIK 240
DB 181 SLMEKIGPNVASLPHILQTDHCQOTHPRADPNRRRTNEPOKLVLLRNLRGGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247
```

## RESULT 2

ID AAB23264 standard; protein; 247 AA.

```
AC AAB23264;
AC 02-FEB-2001 (first entry)
DE Human stannocalcin.
KW Human; stannocalcin; STC; osteogenesis; bone disease; osteoporosis;
KW mineral metabolism regulator; prophylaxis; therapy.
XX Homo sapiens.
XX JP2000229880-A.
XX 22-AUG-2000.
XX 10-FEB-1999; 99JP-00033262.
XX 10-FEB-1999; 99JP-00033262.
XX (SNOW) SNOW BRAND MILK PROD CO LTD.
XX WPI; 2000-605236/58.
XX DR N-PSDB; AAA97594.
XX An osteogenesis promotor useful in the prevention and/or treatment of
XX bone diseases such as osteoporosis.
XX Example 1; Page 5-6; 6pp; Japanese.
XX The invention relates to a novel osteogenesis-promoting composition which
XX contains stannocalcin (STC) as the active component. Stannocalcin is a
XX possible regulator of mineral metabolism. The composition is useful as a
XX prophylactic and/or therapeutic agent for bone diseases such as
XX osteoporosis. The present sequence represents human stannocalcin which
XX was used in an exemplification of the invention
XX SQ Sequence 247 AA;
```

Query Match 100.0%; Score 1268; DB 3; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9.3e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MLQNSAVLLVIVISASATHEAEQNDVSVPKRSVVAQNSAEVVRCLNSALQVCGAFACL 60

```
DB 1 MLQNSAVLLVIVISASATHEAEQNDVSVPKRSVVAQNSAEVVRCLNSALQVCGAFACL 60
QY 61 ENSTCDTDGMYDICKSFLYSAKFDTOGKAFVKSILKCIANGVTSKYFLAIRRCSFTQRM 120
DB 61 ENSTCDTDGMYDICKSFLYSAKFDTOGKAFVKSILKCIANGVTSKYFLAIRRCSFTQRM 120
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHSNRYNRLVRSLLCEDDVTSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHSNRYNRLVRSLLCEDDVTSTIRD 180
QY 181 SLMEKIGPNVASLPHILQTDHCQOTHPRADPNRRRTNEPOKLVLLRNLRGGEEDSPSHIK 240
DB 181 SLMEKIGPNVASLPHILQTDHCQOTHPRADPNRRRTNEPOKLVLLRNLRGGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247
```

## RESULT 3

ID AAY55750 standard; protein; 247 AA.

```
AC AAY55750;
AC 11-FEB-2000 (first entry)
DE Human stannocalcin polypeptide.
XX Stannocalcin-alpha polypeptide; teleocalcin; hypocalcin; hypercalcemic;
XX anti-hypercalcemic glycoprotein hormone; corpuscles of stannus; PTH;
XX parathyroid hormone; bone resorption; osteoporosis; gene therapy; bone;
XX electrolyte disorder; renal; heart disease; osteopetrosis; human;
XX Paget's disease; hypercalcemia.
XX Homo sapiens.
XX US5994103-A.
XX 30-NOV-1999.
XX 02-JUN-1995; 95US-00460529.
XX 10-NOV-1994; 94MO-US013206.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Fleischmann RD, Olsen HS;
XX WPI; 2000-038260/03.
```

Isolated nucleic acids encoding human stannocalcin-alpha useful for  
treating electrolyte disorders which lead to renal, bone and heart  
diseases, osteoporosis and Paget's disease.

Disclosure; Fig 3; 21pp; English.

The invention provides a human stannocalcin-alpha polypeptide (also  
called teleocalcin and hypocalcin). Stannocalcin-alpha is an anti-  
hypercalcemic glycoprotein hormone produced by the corpuscles of  
stannus. It has a similar reported biological activity to that of  
parathyroid hormone (PTH) and both these proteins exhibit dual functions  
in mammals. They exert hypercalcemic activity due to stimulation of bone  
resorption. Further PTH has a biphasic action on bone metabolism (i.e.  
at low doses it increases bone formation and at high doses it increases  
bone resorption. Accordingly, human stannocalcin-alpha and antagonists  
of it (under different circumstances) may be used to treat osteoporosis.  
The DNA may be used to produce human stannocalcin-alpha according to  
standard recombinant DNA methodologies. The human stannocalcin-alpha may  
be produced either in vitro in a fermentation culture or in vivo as part  
of a gene therapy protocol, and may be used to treat electrolyte  
disorders which lead to renal, bone and heart diseases. Due to the

CC biphasic nature of stanniocalcin-alpha it may be used to treat  
CC osteoporosis, osteopetrosis and Paget's disease. Alternatively, the  
CC polypeptides may be used as antigens in the production of antibodies to  
CC stanniocalcin-alpha and to assay for agonists and antagonists of its  
CC activity. The antibodies and antagonists may be used to inhibit the  
CC activity of stanniocalcin-alpha and may be used to treat osteoporosis and  
CC hypercalcaemia. The present sequence represents a human stanniocalcin  
XX  
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9,3e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVIVISATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVGGCAFACL 60  
DB 1 MLQNSAVLLVIVISATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVGGCAFACL 60  
QY 61 ENSTCDTDMGWDICKSFLYSAAKFDTGKAFVYESLKCIANGVTSKVFIAIRCGSTFGQM 120  
DB 61 ENSTCDTDMGWDICKSFLYSAAKFDTGKAFVYESLKCIANGVTSKVFIAIRCGSTFGQM 120  
QY 121 IAEVQEECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD 180  
DB 121 IAEVQEECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD 180  
QY 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGGEDESPSHIK 240  
DB 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGGEDESPSHIK 240  
QY 241 RTSHESA 247  
DB 241 RTSHESA 247

## RESULT 4

AA57166  
ID AAY57166 standard; protein; 247 AA.

XX AAY57166;

DT 11-FEB-2000 (first entry)

XX Human corpuscles of stanius polypeptide.

XX Corpuscles of stanius polypeptide; calcium; inhibition; human; renal;  
XX therapeutic; bone; heart disease; hypocalcaemia; osteoporosis.

XX Homo sapiens.

XX US5994301-A.

XX 30-NOV-1999.

XX 28-APR-1995; 95US-00431117.

XX 08-MAR-1994; 94US-00208005.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Adams MD, Olsen HS;

XX WPI, 2000-038269/03.

XX N-PSDB; AAZ39520.

XX Human corpuscles of stanius polypeptides used to inhibit calcium uptake.  
XX  
XX Claim 4; Fig 1A-B; 23pp; English.

XX This represents a human corpuscles of stanius polypeptide, having a  
XX calcium uptake inhibitory activity. The cDNA is deposited under the  
XX accession number ATCC Deposit No. 75652. The polypeptide can be used in a  
XX method for the treatment of a patient having need to inhibit uptake of

CC calcium. The method is also used for the therapeutic treatment of renal,  
CC bone, and heart diseases, and the antagonist (may be an antibody) may be  
CC used for treating hypocalcaemia, and osteoporosis  
XX  
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9,3e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVIVISATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVGGCAFACL 60  
DB 1 MLQNSAVLLVIVISATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVGGCAFACL 60  
QY 61 ENSTCDTDMGWDICKSFLYSAAKFDTGKAFVYESLKCIANGVTSKVFIAIRCGSTFGQM 120  
DB 61 ENSTCDTDMGWDICKSFLYSAAKFDTGKAFVYESLKCIANGVTSKVFIAIRCGSTFGQM 120  
QY 121 IAEVQEECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD 180  
DB 121 IAEVQEECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD 180  
QY 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGGEDESPSHIK 240  
DB 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGGEDESPSHIK 240  
QY 241 RTSHESA 247  
DB 241 RTSHESA 247

## RESULT 5

AA52901  
ID AAY2901 standard; protein; 247 AA.

XX AAY2901;

DT 26-SEP-2000 (first entry)

XX Human stanniocalcin protein.

XX PCR primer; human; stanniocalcin; inhibitor; differentiation; maturation;  
XX adipocyte; obesity; diabetes; hypertension; heart disease.

XX Homo sapiens.

XX WO200016795-A1.

XX 30-MAR-2000.

XX 17-SEP-1999; 99WO-JP005080.

XX 17-SEP-1998; 98JP-00263004.

XX (SNOW) SNOW BRAND MILK PROD CO LTD.

XX Goto M, Tomoyasu A, Yamaguchi K, Kinoshita M, Nakagawa N;

XX WPI, 2000-283445/24.

XX N-PSDB; AAA11145.

XX Treating or preventing obesity, which is a risk factor for diabetes,  
XX hypertension and heart disease, comprises administering an agent  
XX containing stanniocalcin.

XX Example 1; Page 16; 19pp; Japanese.

XX This sequence represents the human stanniocalcin protein. Stanniocalcin  
XX is an inhibitor of the differentiation and maturation of adipocytes. The  
XX protein is used for preventing and treating obesity which is a risk  
XX factor for diabetes, hypertension, and heart disease. The coding sequence  
XX was isolated from IMR-90 cells



XX MPI: 2001-316386/33.  
 DR N-PSDB; AAF83823.  
 XX  
 PT Novel assay for diagnosing and monitoring cancer, involves determining  
 PT levels of lng108 in cells, tissues or bodily fluids of the patient, and  
 PT comparing with control.  
 XX

PS Disclosure; Page 33-34; 36pp; English.

XX The invention relates to diagnosing the presence of cancer or diagnosing  
 CC metastases of cancer in a patient that involves determining levels of  
 CC lng108 in a sample of cells, tissues or bodily fluids in a patient, and  
 CC comparing the determined levels with levels of lng108 a normal human  
 CC control. The method is useful for diagnosing the presence of cancer.  
 CC diagnosing metastases of cancer, staging cancer, monitoring cancer, and  
 CC monitoring a change in stage of the cancer, in a patient. A therapeutic  
 CC agent which is an antibody labeled with paramagnetic ions or a  
 CC radioisotope, and conjugated with a cytotoxic agent is useful for imaging  
 CC cancer in a patient. A molecule which downregulates the expression or  
 CC activity of lng108, is useful for treating cancer in a patient. lng108  
 CC protein is useful for inducing an immune response against a target cell  
 CC expressing lng108. The present sequence represents the human lng108  
 CC polypeptide  
 CC  
 XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 4; Length 247;

Best Local Similarity 100.0%; Pred. No. 9.3e-124; Mismatches 0; Gaps 0;

Matches 247; Conservative 0; Indels 0; Gaps 0;

QY 1 MQNSAVLVLVISASATHEAEQNDVSPPKRSVAQAQNSAEVVRCLNSALQVGGAFACL 60  
 DB 1 MQNSAVLVLVISASATHEAEQNDVSPPKRSVAQAQNSAEVVRCLNSALQVGGAFACL 60  
 QY 61 ENSTCTDGMVDICKSPFYSAKPDTOGKAFVKSILKCIANGVSKVFLAIRCSTFGRM 120  
 DB 61 ENSTCTDGMVDICKSPFYSAKPDTOGKAFVKSILKCIANGVSKVFLAIRCSTFGRM 120  
 QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFNSRYNRLVRSLLCEDDTVSTIRD 180  
 DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFNSRYNRLVRSLLCEDDTVSTIRD 180  
 QY 181 SIEMKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLRGEEDSPSHIK 240  
 DB 181 SIEMKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLRGEEDSPSHIK 240  
 QY 241 RTSHESA 247  
 DB 241 RTSHESA 247

RESULT 8

ABP06259  
 ID ABB06259 standard; protein; 247 AA.

AC ABB06259;

DT 23-MAY-2002 (first entry)

DE Human stanoicacin 1 protein.

XX Human, stanoicacin 1; osteopathic; osteogenesis failure; osteoporosis;  
 KW bone mass reduction; traumatic bone injury; osteomalacia; bone disease;  
 KW rheumatic bone disease; cancer associated bone disease; rachitis;  
 KW arthritis deformans.

OS Homo sapiens.

PN WO200204013-A1.

PD 17-JAN-2002.

PF 10-JUL-2001; 2001WO-JP005962.

XX 11-JUL-2000; 2000JP-00209926.

XX (BMLB-) BML INC.

PI Yoshiko Y, Koide Y, Igarashi A, Takano S, Maeda N, Aubin JE;

DR MPI: 2002-164600/21.

XX N-PSDB; ABL40225.

PT Agent used for treating bone diseases e.g. osteoporosis, traumatic bone  
 PT injury, osteomalacia, rheumatic bone diseases, bone diseases associated  
 PT with cancer and arthritis deformans containing stanoicacin I.

PS Claim 2; Fig 1; 24pp; Japanese.

XX The present invention describes an agent containing stanoicacin 1,  
 CC particularly of human origin. Stanoicacin 1 has osteopathic activity.  
 CC The agent can be used for treating diseases relating to osteogenesis  
 CC failure or reduction in bone mass e.g. osteoporosis, traumatic bone  
 CC injury, osteomalacia, rheumatic bone diseases, bone diseases associated  
 CC with cancer, bone diseases due to phosphorus or calcium metabolic error,  
 CC rachitis and arthritis deformans. The agent increases bone mass. The  
 CC present sequence represents human stanoicacin 1  
 CC  
 XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 5; Length 247;

Best Local Similarity 100.0%; Pred. No. 9.3e-124; Mismatches 0; Gaps 0;

QY 1 MQNSAVLVLVISASATHEAEQNDVSPPKRSVAQAQNSAEVVRCLNSALQVGGAFACL 60  
 DB 1 MQNSAVLVLVISASATHEAEQNDVSPPKRSVAQAQNSAEVVRCLNSALQVGGAFACL 60  
 QY 61 ENSTCTDGMVDICKSPFYSAKPDTOGKAFVKSILKCIANGVSKVFLAIRCSTFGRM 120  
 DB 61 ENSTCTDGMVDICKSPFYSAKPDTOGKAFVKSILKCIANGVSKVFLAIRCSTFGRM 120  
 QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFNSRYNRLVRSLLCEDDTVSTIRD 180  
 DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFNSRYNRLVRSLLCEDDTVSTIRD 180  
 QY 181 SIEMKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLRGEEDSPSHIK 240  
 DB 181 SIEMKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLRGEEDSPSHIK 240  
 QY 241 RTSHESA 247  
 DB 241 RTSHESA 247

RESULT 9

ABP97748  
 ID ABP97748 standard; protein; 247 AA.

AC ABP97748;

DT 28-MAY-2003 (first entry)

DE Amino acid sequence of human STC1 polypeptide.

XX Human; angiogenesis; wound healing; retinopathy; ischemia; inflammation;  
 KW microvasculopathy; bone healing; skin inflammation; HOG3; HOG18;  
 KW follicular development; CAG; HXB; IGBP5; HFAF; STC1; mlg-6; SSR4;  
 KW cancer.

OS Homo sapiens.

PN WO2003010205-A1.

PD 06-FEB-2003.

XX 26-JUN-2002; 2002WO-US023786.  
XX  
XX 26-JUL-2001; 2001US-0307600P.  
XX 24-JUL-2002; 2002US-00201642.  
XX  
XX (UYDU-) UNIV DUKE MEDICAL CENT.  
XX  
XX Riggs GJ, Lal A;  
XX WPI, 2003-239423/23.  
XX N-PSDB; AB277288.  
XX  
XX Inhibiting angiogenesis for treating wound healing, retinopathy,  
XX ischemia, inflammation, microvasculopathy, bone healing, skin  
XX inflammation or follicular development by providing to a subject an  
XX antitense polynucleotide.  
XX  
XX Claim 4; Page 61; 66pp; English.  
XX  
XX The present sequence is a human STC1 polypeptide. It is used in the  
XX method of the invention. The specification describes a method modulating  
XX angiogenesis associated with wound healing, retinopathy, ischemia,  
XX inflammation, microvasculopathy, bone healing, skin inflammation or  
XX follicular development. The method comprises providing to a subject HOG3,  
XX HOG8, HOG18, CA9, HXB, IGFBP5, HPARP, STC1, mig-6 or SSR4. The methods,  
XX antitense polynucleotides, polypeptides and antibodies are useful for  
XX treating wound healing, retinopathy, ischemia, inflammation,  
XX microvasculopathy, bone healing, skin inflammation or follicular  
XX development, or cancer such as breast, colon or lung cancer, or  
XX glioblastoma  
XX  
XX Sequence 247 AA;  
XX  
XX Query Match 100.0%; Score 1268; DB 6; Length 247;  
XX Best Local Similarity 100.0%; Pred. No. 9, 3e-124;  
XX Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGNASAVLLVIVISASATHEAEQNDVSFPRKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60  
DB 1 MGNASAVLLVIVISASATHEAEQNDVSFPRKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60  
QY 61 ENSTCDTDGMYDICKSFVSAKFTDQGAFFVESIKCIANGVTSKVFLAIRCSTFORM 120  
DB 61 ENSTCDTDGMYDICKSFVSAKFTDQGAFFVESIKCIANGVTSKVFLAIRCSTFORM 120  
QY 121 IAEVQECYSKLNWCSIAKRNPEAITVEVQLPNHFSNRYNRLVRSLLCEDEDVTSTIRD 180  
DB 121 IAEVQECYSKLNWCSIAKRNPEAITVEVQLPNHFSNRYNRLVRSLLCEDEDVTSTIRD 180  
QY 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGGEEDSPSHIK 240  
DB 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGGEEDSPSHIK 240  
QY 241 RTSHESA 247  
DB 241 RTSHESA 247  
RESULT 10  
ABR47600  
ID ABR47600 standard; protein; 247 AA.  
XX  
XX ABR47600;  
XX  
XX 12-JUN-2003 (first entry)  
XX  
XX Breast cancer associated protein sequence SEQ ID NO:441.  
XX  
XX Human; breast cancer; cytostatic; gene therapy.  
XX  
XX Homo sapiens.  
XX

PN WO2003004989-A2.  
XX  
XX 16-JAN-2003.  
XX  
XX 21-JUN-2002; 2002WO-US019669.  
XX  
XX 21-JUN-2001; 2001US-0299887P.  
XX 27-JUN-2001; 2001US-0301572P.  
XX 18-JUN-2001; 2001US-0306501P.  
XX 25-SEP-2001; 2001US-0325002P.  
XX 05-MAR-2002; 2002US-0362855P.  
XX 14-MAY-2002; 2002US-0360391P.  
XX  
XX (MILL-) MILLENIUM PHARM INC.  
XX  
XX Lillie J, Gannavarapu M, Glatz K, Hoerth S, Kamatkar S;  
XX Mertens M, Monahan DE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;  
XX Baer RC, Hortobagyi GN, Fuzetla L, Welle F, Sahni A, Mills GB;  
XX WPI; 2003-210381/20.  
XX N-PSDB; ACC50301.  
XX  
XX Breast cancer diagnosis or treatment by comparing the level of expression  
XX of a marker in a patient sample with that in the control non-breast  
XX cancer sample.  
XX  
XX Claim 1; SEQ ID NO 441; 128pp; English.  
XX  
XX The present invention describes a method for assessing whether a patient  
XX is afflicted with breast cancer. The method comprises comparing the level  
XX of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and  
XX ABR47386 to ABR47632) in a patient sample and the normal level of  
XX expression of the marker in a control non-breast cancer sample, where a  
XX significant increase in the level of expression of the marker in the  
XX patient sample and the normal level is an indication that the patient is  
XX afflicted with breast cancer. The breast cancer associated sequences from  
XX the present invention have cytostatic activities and can be used in gene  
XX therapy. The method is useful for diagnosing and treating breast cancer.  
XX N.B. The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pot\_sequences  
XX  
XX Sequence 247 AA;  
XX  
XX Query Match 100.0%; Score 1268; DB 6; Length 247;  
XX Best Local Similarity 100.0%; Pred. No. 9, 3e-124;  
XX Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGNASAVLLVIVISASATHEAEQNDVSFPRKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60  
DB 1 MGNASAVLLVIVISASATHEAEQNDVSFPRKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60  
QY 61 ENSTCDTDGMYDICKSFVSAKFTDQGAFFVESIKCIANGVTSKVFLAIRCSTFORM 120  
DB 61 ENSTCDTDGMYDICKSFVSAKFTDQGAFFVESIKCIANGVTSKVFLAIRCSTFORM 120  
QY 121 IAEVQECYSKLNWCSIAKRNPEAITVEVQLPNHFSNRYNRLVRSLLCEDEDVTSTIRD 180  
DB 121 IAEVQECYSKLNWCSIAKRNPEAITVEVQLPNHFSNRYNRLVRSLLCEDEDVTSTIRD 180  
QY 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGGEEDSPSHIK 240  
DB 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGGEEDSPSHIK 240  
QY 241 RTSHESA 247  
DB 241 RTSHESA 247  
RESULT 11  
ABG72290  
ID ABG72290 standard; protein; 247 AA.  
XX



AC ABG72290;  
 XX  
 DT 14-MAR-2003 (first entry)  
 XX  
 XX Human Corpuscles of Stannius protein.  
 XX  
 KM Human; Corpuscles of Stannius protein; calcium uptake inhibitor;  
 KM renal excretion of phosphate; electrolyte disorder; renal disease;  
 KM bone disease; heart disease; arterial hypertension; bone resorption;  
 KM osteoporosis; Paget's disease; hypercalcaemia; hyperparathyroidism;  
 KM hypervitaminosis D; tumour; serum calcium level; sarcoidosis;  
 KM hyperthyroidism; adrenal insufficiency; serum albumin; plasma protein;  
 KM Gi calcium absorption; stannocalcin; osteopathic; cytostatic;  
 KM hypotensive.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002146791-A1.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PP 05-APR-2002; 2002US-00116051.  
 XX  
 XX 08-MAR-1994; 94US-00208005.  
 PR 28-APR-1995; 95US-00431117.  
 PR 17-MAY-1999; 99US-00312610.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Olsen HS, Adams MD;  
 XX  
 DR MPI; 2003-147579/14.  
 DR N-PSDB; ABX15152.  
 XX  
 PT Isolated polynucleotide for encoding polypeptides used to diagnose and  
 PT treat electrolyte disorders leading to renal disease, e.g. Paget's  
 PT disease, hypercalcaemia and sarcoidosis.  
 XX  
 PS Claim 13; Fig 1; 26pp; English.  
 XX  
 CC The present invention relates to the isolation of human Corpuscles of  
 CC Stannius protein, and the polynucleotide sequence encoding it. Human  
 CC Corpuscles of Stannius protein inhibits calcium uptake and reduces renal  
 CC excretion of phosphate. The polynucleotide sequence is useful for  
 CC encoding Corpuscles of Stannius protein for therapeutic purposes, e.g. in  
 CC the treatment of electrolyte disorders that lead to renal, bone or heart  
 CC disease, such as arterial hypertension, disorders due to elevated bone  
 CC resorption (e.g. osteoporosis and Paget's disease), and hypercalcaemia  
 CC (e.g. hyperparathyroidism, hypervitaminosis D), tumours that raise serum  
 CC calcium levels by destroying bone, sarcoidosis, hyperthyroidism, adrenal  
 CC insufficiency, loss of serum albumin secondary to renal diseases, or  
 CC excessive Gi calcium absorption and elevated concentration of plasma  
 CC proteins. The encoded polypeptide exhibits a high degree of homology to  
 CC stannocalcin from *Anguilla australis* and from *Oncorhynchus kisutch*. The  
 CC present sequence represents human corpuscles of stannius protein  
 XX  
 XX Sequence 247 Aa;  
 SQ  
 Query Match 100.0%; Score 1268; DB 6; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-124;  
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 SLMEKIGFNMASTPHILQTDHCAQTHPRADFNRRRTNEPQTKYLINLRGEEDSPSHIK 240  
 |||||  
 DB 181 SLMEKIGFNMASTPHILQTDHCAQTHPRADFNRRRTNEPQTKYLINLRGEEDSPSHIK 240  
 QY 241 RTSHESA 247  
 |||||  
 DB 241 RTSHESA 247  
 RESULT 12  
 ADD48082  
 ID ADD48082 standard; protein; 247 AA.  
 XX  
 AC ADD48082;  
 XX  
 XX 29-JAN-2004 (first entry)  
 DT  
 XX  
 DE Human Protein P52823, SEQ ID NO 13779.  
 XX  
 KM Human; pain; neuronal tissue; gene therapy;  
 KM spinal segmental nerve injury; chronic constriction injury; CCI;  
 KM spared nerve injury; SNJ; Chung.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO2003016475-A2.  
 PN  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 14-AUG-2002; 2002WO-US025765.  
 XX  
 PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-033347P.  
 XX  
 PA (GENO) GEN HOSPITAL CORP.  
 PA (FARB) BAYER AG.  
 XX  
 PI Woolf C, D'urso D, Bofort K, Costigan M;  
 XX  
 DR MPI; 2003-268312/26.  
 DR GENBANK; F52823.  
 XX  
 PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX  
 PS Claim 1; Page; 1017pp; English.  
 XX  
 CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNJ)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a human protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:

CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pat\_sequences.

XX Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 7; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9, 3e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLONSAVLVIVISASATHEAEONDSVSPKRSVVAQNSAEVVRCLNSALQVCGAFACL 60  
DB 1 MLONSAVLVIVISASATHEAEONDSVSPKRSVVAQNSAEVVRCLNSALQVCGAFACL 60  
QY 61 ENSTCDTDMGYDICKSFLYSAAKPTQGAFFVESLKCIANGVTSKVFIAIRCSFTFORM 120  
DB 61 ENSTCDTDMGYDICKSFLYSAAKPTQGAFFVESLKCIANGVTSKVFIAIRCSFTFORM 120  
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180  
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180  
QY 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGSEDSPSHIK 240  
DB 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGSEDSPSHIK 240  
QY 241 RTSHESA 247  
DB 241 RTSHESA 247

## RESULT 13

AD130575  
ID AD130575 standard; protein; 247 AA.

XX AC AD130575;  
DT 22-APR-2004 (first entry)  
XX Human stannocalcin protein.  
XX human; stannocalcin-alpha; electrolyte imbalance; hypertension;  
KW hyperglycaemia; migraine; renal disease; heart disease;  
KW osteoporosis; hypoglycaemia; Paget's disease.  
XX OS Homo sapiens.  
PN US2003181663-A1.  
XX PD 25-SEP-2003.  
XX PF 18-APR-2003; 2003US-00418226.  
XX PR 10-NOV-1994; 94MO-US013206.  
XX PR 02-JUN-1995; 95US-00460529.  
XX PR 28-JUL-1999; 99US-00361736.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
PI Olsen HS, Fleischmann RD;  
XX WPI; 2003-852260/79.  
XX New human stannocalcin-alpha polypeptide, useful in regulating  
PT electrolyte imbalances, or for diagnosing and treating a disease  
PT associated with mutated forms of stannocalcin-alpha sequences, e.g.  
PT renal disease or osteoporosis.  
XX PS Disclosure; SEQ ID NO 10; 22pp; English.  
XX The invention comprises the amino acid and coding sequence of a human  
CC stannocalcin-alpha protein. The DNA and protein sequences of the  
CC invention are useful for regulating electrolyte imbalances to treat

CC hypertension, hyperglycaemia or migraine. The DNA and protein sequences  
CC are also useful in diagnosing and treating a disease associated with  
CC mutated forms of stannocalcin-alpha sequences, such as: renal disease,  
CC heart disease or bone disease (e.g. osteoporosis). The DNA and protein  
CC sequences may also be used to treat hypoglycaemia or Paget's disease. The  
CC present amino acid sequence represents a human stannocalcin protein.

XX Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 7; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9, 3e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLONSAVLVIVISASATHEAEONDSVSPKRSVVAQNSAEVVRCLNSALQVCGAFACL 60  
DB 1 MLONSAVLVIVISASATHEAEONDSVSPKRSVVAQNSAEVVRCLNSALQVCGAFACL 60  
QY 61 ENSTCDTDMGYDICKSFLYSAAKPTQGAFFVESLKCIANGVTSKVFIAIRCSFTFORM 120  
DB 61 ENSTCDTDMGYDICKSFLYSAAKPTQGAFFVESLKCIANGVTSKVFIAIRCSFTFORM 120  
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180  
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180  
QY 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGSEDSPSHIK 240  
DB 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGSEDSPSHIK 240  
QY 241 RTSHESA 247  
DB 241 RTSHESA 247

## RESULT 14

ABO84399  
ID ABO84399 standard; protein; 247 AA.

XX AC ABO84399;  
DT 29-JUL-2004 (first entry)  
XX Human stannocalcin protein.  
XX Human; antihypertensive; bronchoconstriction; allergy; hyposecretion; pain;  
KW respiratory tract inflammation; adenosine sensitivity; lung cancer;  
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KW pulmonary transplantation rejection.  
XX OS Homo sapiens.  
PN WO200285309-A2.  
XX PD 31-OCT-2002.  
XX PF 23-APR-2002; 2002MO-US013143.  
XX PR 24-APR-2001; 2001US-0286036P.  
XX PA (EPIG-) EPIGENESIS PHARM INC.  
PI Nyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahbuddin S;  
XX WPI; 2003-093056/08.  
XX N-PSDB; ABD20397.  
XX Pharmaceutical composition for treating asthma, has antihypertensive  
PT oligonucleotide containing less percentage of adenosine, targeted to

PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.

XX Claim 15; SEQ ID NO 6; 763bp; English.

CC This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has anti-allergic, anti-inflammatory, anti-asthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to  
CC prevent any unwanted effects due to it

XX Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 7; Length 247;

Best Local Similarity 100.0%; Pred. No. 9.3e-124; Indels 0; Gaps 0;

Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNASAVLVIVISASATHEAEONDSVSPKRSVAAQNSAEVRCINSALQVCGCAFACL 60  
DB 1 MGNASAVLVIVISASATHEAEONDSVSPKRSVAAQNSAEVRCINSALQVCGCAFACL 60  
QY 61 ENSTCDTGMVDICSFYSAKFDTOGKAFVKSILKCIANGVTSKVFIAIRRCSTFGQM 120  
DB 61 ENSTCDTGMVDICSFYSAKFDTOGKAFVKSILKCIANGVTSKVFIAIRRCSTFGQM 120  
QY 121 IAEVOECYSKLNVCSIAKRNPEAITTEVQLPNHFNSRNYRLVRSLLCEDEDTVSTIRD 180  
DB 121 IAEVOECYSKLNVCSIAKRNPEAITTEVQLPNHFNSRNYRLVRSLLCEDEDTVSTIRD 180  
QY 181 SLMEKIGPNMASLFPHILOTCHCAQTHPRADFNRRRTNEPQKLKYLRLNREEDSPSHIK 240  
DB 181 SLMEKIGPNMASLFPHILOTCHCAQTHPRADFNRRRTNEPQKLKYLRLNREEDSPSHIK 240  
QY 241 RTSHESA 247  
DB 241 RTSHESA 247

RESULT 15

ADQ21382 standard; protein; 247 AA.

AC ADQ21382;

DT 26-AUG-2004 (first entry)

DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4202.

XX

KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.

XX Homo sapiens.

XX WO2004048938-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US038193.

XX 26-NOV-2002; 2002US-0429739P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Aziz N, Ginsburg WM, Zlotnik A;

XX WPI; 2004-441208/41.

PT Early detection of soft tissue sarcoma comprises determining expression  
PT of a gene in a first soft tissue sample and a normal soft tissue sample  
PT and comparing the gene expression, also useful in treating soft tissue  
PT sarcoma.

PS Example 2; SEQ ID NO 4202; 210bp; English.

CC The invention relates to a novel method for detecting soft tissue sarcoma  
CC which comprises obtaining a first soft tissue sample from an individual  
CC and a normal soft tissue sample from the same or different individual,  
CC determining the expression of a gene in both samples and comparing the  
CC expression of the gene in both soft tissue samples, where a higher level  
CC of protein expression in the first soft tissue sample indicates the  
CC presence of soft tissue sarcoma. The method of the invention has  
CC cytostatic applications and may be useful for detecting soft tissue  
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
CC acid sequences may be useful in diagnostic and screening applications.  
CC The current sequence is that of a human soft tissue sarcoma-upregulated  
CC protein of the invention. The current sequence is not shown within the  
CC specification per se but was submitted in CD format by the inventor.

XX Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 8; Length 247;

Best Local Similarity 100.0%; Pred. No. 9.3e-124; Indels 0; Gaps 0;

Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNASAVLVIVISASATHEAEONDSVSPKRSVAAQNSAEVRCINSALQVCGCAFACL 60  
DB 1 MGNASAVLVIVISASATHEAEONDSVSPKRSVAAQNSAEVRCINSALQVCGCAFACL 60  
QY 61 ENSTCDTGMVDICSFYSAKFDTOGKAFVKSILKCIANGVTSKVFIAIRRCSTFGQM 120  
DB 61 ENSTCDTGMVDICSFYSAKFDTOGKAFVKSILKCIANGVTSKVFIAIRRCSTFGQM 120  
QY 121 IAEVOECYSKLNVCSIAKRNPEAITTEVQLPNHFNSRNYRLVRSLLCEDEDTVSTIRD 180  
DB 121 IAEVOECYSKLNVCSIAKRNPEAITTEVQLPNHFNSRNYRLVRSLLCEDEDTVSTIRD 180  
QY 181 SLMEKIGPNMASLFPHILOTCHCAQTHPRADFNRRRTNEPQKLKYLRLNREEDSPSHIK 240  
DB 181 SLMEKIGPNMASLFPHILOTCHCAQTHPRADFNRRRTNEPQKLKYLRLNREEDSPSHIK 240  
QY 241 RTSHESA 247  
DB 241 RTSHESA 247

Search completed: November 16, 2004, 09:56:01  
Job time : 155 secs

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: November 16, 2004, 08:03:25 ; Search time 418 Seconds  
(without alignment)

6693.992 Million cell updates/sec

Title: US-09-703-350B-75  
Perfect score: 6832  
Sequence: 1 cagtttcgcaaaagccagag.....aaaaaaaaaaaaaaaa 3900

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2002273 segs, 35872929 residues

Total number of hits satisfying chosen parameters: 4004546

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+n2p-model -DSV=klp  
-Q=/cgn2/\_USPTO.spool\_P/US0970330/runat.16112004.080315.14039/app.query.fasta.1.4039  
-DB=A\_Geneseq\_23Sep04 -QFM=fastan -SUFFIX=rag -MINMATCH=0.1 -DOOPCL=0  
-LIST=45 -DOCLALIGN=200 -START=1 -END=-1 -MATRIX=blsum62 -TRANS=human40.cdi  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09703350 @CNC 1.1 570 @runat.16112004.080315.14039 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -IONCLOG  
-DEV\_TIMEOUT=120 -MAIN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq\_23Sep04:.\*  
1: geneseqp1980s:.\*  
2: geneseqp1990s:.\*  
3: geneseqp2000s:.\*  
4: geneseqp2001s:.\*  
5: geneseqp2002s:.\*  
6: geneseqp2003as:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1403	20.5	276	3	AAB56848 Human pro
2	1268	18.6	247	2	AAB84522 Stannoca
3	1268	18.6	247	3	AAB23264 Human sta
4	1268	18.6	247	3	AAY55750 Human sta
5	1268	18.6	247	3	AAY57166 Human cor
6	1268	18.6	247	3	AAY92901 Human sta
7	1268	18.6	247	4	AAB62473 Human sta
8	1268	18.6	247	4	AAB62690 Ling108, a
9	1268	18.6	247	5	ABB06259 Human sta
10	1268	18.6	247	6	ABP97748 Amino aci

11	1268	18.6	247	6	ABR47600 Breast ca
12	1268	18.6	247	6	ABG72290 Human cor
13	1268	18.6	247	7	ADD48082 Human pro
14	1268	18.6	247	7	AD130575 Human sta
15	1268	18.6	247	7	AB084399 Human sta
16	1268	18.6	247	8	ADQ21382 Human sot
17	1231	18.0	247	7	ADD48080 Rat Prote
18	696.5	10.2	261	1	AAP82968 Corpucle
19	662.5	9.7	256	4	AAB62474 Coho salm
20	628	9.2	170	3	AAY55749 A. austri
21	628	9.2	170	3	AD130574 Australia
22	362	5.3	302	3	AAY67925 Human sta
23	362	5.3	302	4	AAB96971 Human adi
24	362	5.3	302	4	AAB61621 Human sta
25	362	5.3	302	4	AAB31797 Amino aci
26	362	5.3	302	4	AAB95330 Human pro
27	362	5.3	302	5	ABJ05546 Breast ca
28	362	5.3	302	5	AAB26113 Human BS2
29	362	5.3	302	6	AAB47601 Breast ca
30	362	5.3	302	6	ADA00844 Human bre
31	362	5.3	302	7	ADA27593 Human sta
32	362	5.3	302	7	ADB80516 Ovarian c
33	362	5.3	302	7	AD130577 Human sta
34	362	5.3	302	7	ADN38782 Cancer/an
35	362	5.3	302	8	ADO28591 Human sta
36	358	5.2	70	4	AAM18134 Peptide #
37	358	5.2	70	4	ABR37166 Peptide #
38	358	5.2	70	4	AAM30637 Peptide #
39	358	5.2	70	4	ABR31928 Peptide #
40	358	5.2	70	4	ABB22472 Protein #
41	358	5.2	70	4	AAY70300 Human bon
42	358	5.2	70	4	AAW57878 Human bra
43	358	5.2	70	4	ABG52000 Human liv
44	358	5.2	70	4	AAM05763 Peptide #
45	358	5.2	70	5	ABG39940 Human pep

#### ALIGNMENTS

RESULT 1  
AAB56848 standard: protein; 276 AA.

ID AAB56848  
AC AAB56848;  
DT 13-MAR-2001 (first entry)  
XX Human prostate cancer antigen protein sequence SEQ ID NO:1426.  
DE Human prostate cancer antigen: detection; diagnosis;  
KW Human; prostate cancer; prostate cancer antigen; immunomodulatory; muscular;  
KW neuroprotective; cytoskeletal; cardiovascular; nephrotoxic; antineoplastic;  
KW vulntrary; gastrointestinal; nephrotoxic; antineoplastic; gynaecological;  
KW antibacterial; gene therapy; immune; reproductive; renal;  
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
KW wound; infectious disease.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200055174-A1.  
XX  
XX PD 21-SEP-2000.  
XX  
XX PF 08-MAR-2000; 2000MO-US005988.  
XX  
XX PR 12-MAR-1999; 99US-0124270P.  
XX  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX (ROSE/) ROSEN C A.  
XX  
XX PI Rosen CA, Ruben SM;  
XX WPI, 2000-587513/55.  
XX DR N-PSDB; AAF16051.











Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	18.56%	Indels:	0
DB:	3	Gaps:	0

QY	28	ATGCTCAAAACCTCAGCAGGCTCTGGGCTGGGATCAAGGCTTGCACACCATGAG	34
Db	1	MeLeuGlnHisSerHisValLeuLeuValLeuValIleSerHisSerHisIleHisGlu	20
QY	345	GCGAGAGAGATGACTCTGTGTGAGCCCCAGAAATCCGAGTGGCGGCTCAAAATCAGCT	404
Db	21	AlaGlnGlnHisSerHisValSerProArgLysSerArgValAlaAlaGlnHisSerHis	40
QY	405	GAGTGGTTCGGTTCCTCAACAGTGGTCTACAGAGCTCGGCTGGGGGCTTTGGATGGCTG	464
Db	41	GluValValArgCysLeuHisSerHisAlaLeuGlnValIleGlySerGlyAlaHisCysLeu	60
QY	465	GAATACTCAACTCTGTGACACAGATGGATGATGACATCTGTAATCTTGTGTACAGC	524
Db	61	GlnHisSerHisCysAspHisAspGlyMetCysAspIleCysLysSerHisLeuTyrSer	80
QY	525	GCTGCTAAATTTTGACACTCAGAGGAAAGATTCGCAAGAGAGATTAAATGATGACGC	584
Db	81	AlaHisLysPheAspHisPheGlnLysLysAlaPheValLysGlnSerLeuLysCysIleAla	1000
QY	585	AACGGGATCACTCCAAAGGCTCTTCTCGCAATCGAGGTCTCCACTTCGAAAGATG	644
Db	101	AsnGlyValAlaHisSerLysValPheLeuAlaIleArgArgCysSerHisPheGlnArgMet	120
QY	645	ATTGCTGAGGTGCAGGAGAGAGGTCACAGCAAGCTGATGTGTGAGATGCGCAAGCGG	704
Db	121	IleAlaGlnValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	1400
QY	705	AACCTGAAAGCATCATCTGAGGTCGTGACAGCTGCCCAATCATCTTCTCCAAAGATTAAT	764
Db	141	AsnProGlnAlaAlaIleThrGlnValValGlnLeuProHisIlePheSerHisArgTyrTyr	160
QY	765	AACAGACTGTGCGGAAGGCTGTGGAATGTGATGAGAAGCAGACAGACAGATCAGAGAC	824
Db	161	AsnArgLeuValAlaHisSerLeuLeuGlnCysAspGlnAspHisPheValSerHisIleArgAsp	180
QY	825	AGCTGTATGAGAAAAATTGGGCTTAACATGGCGCAGCCTCTTCCACATCTCGACAGAC	884
Db	181	SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp	200
QY	885	CAGCTGGGCCAAACACACCCAGACACTCTTCAACAGAGAACCCACCATGAGCGGACG	944
Db	201	HisCysAlaGlnThrHisIleProArgAlaAspPheHisArgAlaGlnHisArgGlnProGln	220
QY	945	AAGCTGAAAGTCTCTCTCAGGAACCTCCAGAGTGAAGAGACTCTCCCTCCACATCAAA	1000
Db	221	LysLeuLysValLeuLeuArgHisLeuArgGlnGlyGlnGlnAspSerProSerHisIleLys	240
QY	1005	CGCAGATCCCATGAGAGATGCA	1025
Db	241	ArgIleSerHisGlnSerHis	247
RESULT 7			
AAB62473			
AAB62473 standard; protein; 247 AA.			
AAB62473;			
09-UTL-2001 (first entry)			
Human stannocalcin (STC) protein.			
Stannocalcin; STC; neuroprotective; anti-inflammatory; anti-anemic;			
KW anti-thrombotic; anti-atherogenic; dermatological; anti-allelic; human;			
KW nephrotropic; antithyroid; immunosuppressive; antidiabetic; vitreous;			
KW antidiabetic; hemostatic; anti-atherogenic; vasodilator; antiproliferative;			
KW antitumor; anti HIV; antiparkinsonian; neurotropic; cell proliferation;			

XX	hemostatic; thrombolytic.
XX	
OS	Homo sapiens.
XX	
PN	W0200130969-A2.
XX	
PD	03-MAY-2001.
XX	
PF	20-OCT-2000; 2000MO-US029432.
XX	
PR	27-OCT-1999; 99US-0161740P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC. (UYHE-) UNIV HELSINKI.
XX	
PI	Olsen HS, Zhang K, Lindsberg P, Tatlisunak T, Kaete M; Anderson LC;
DR	WPI; 2001-308626/32.
XX	
N-PSDB	AAF83297.
PT	Novel composition useful for treating or protecting neural cells, for treating Addison's disease, organ rejection, hyperproliferative disorder, cancer, AIDS, multiple sclerosis, comprises stannocalcin polypeptide.
XX	
PS	Claim 1; Fig 1A-C; 253pp; English.
CC	The invention relates to a human stannocalcin (STC) polypeptide. A pharmaceutical composition comprising the STC is useful for treating a patient in need of increased levels of STC activity. STC and its modulators are useful for treating disorders or abnormalities of nervous system, cerebrovascular diseases, dementia, encephalitis, central nervous system infections or neoplasms, demyelinating diseases, encephalomyelitis, spinal cord diseases, mental retardation such as Down's syndrome, Tay-Sachs disease, neuromuscular diseases such as muscular dystrophy, myasthenia gravis, deficiencies or disorders of immune system such as Addison's disease, hemolytic anemia, rheumatoid arthritis, dermatitis, glomerulonephritis, Goodpasture's Syndrome, Grave's disease, multiple sclerosis, autoimmune thyroiditis, systemic lupus erythematosus, insulin dependent diabetes mellitus, allergic reactions and conditions such as asthma, for treating and/or preventing organ rejection or graft-versus-host disease, hyperproliferative diseases such as psoriasis, Gaucher's disease, cardiovascular disorders such as arrhythmias, telangiectasia, vasculitis, and for treatment of disease or disorders with neurovascularization. The composition can be used to treat hemangioma, psoriasis, angiodiroma, atherosclerotic plaques, delayed wound healing, granulomas, Osler-Weber syndrome, solid tumors such as Kaposi's sarcoma, cancer, AIDS, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, wound healing, and for treating or detecting infectious agents. The present sequence represents the human STC polypeptide
XX	
XX	Sequence 247 AA:
XX	
Alignment Scores:	
Pred. No.:	6,456-115 Length: 247
Score:	1268.00 Matches: 247
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	18.56% Indels: 0
DB:	Gaps: 0
US-09-703-350B-75 (1-3900) x AAB62473 (1-247)	
OY	285 ATGCTTCAAAATCGACGAGTGCTTTGGTGTGTCATCATGCTTCTTGACCCATGAG 344
D8	 1 MetLeuGlnAsnSerAlaValLeuIleuValIleValIIeSerAlaSerAlaThrHisGlu 20
OY	345 GCGGAGCAGAATGACTCTGTGAGGCCCGCAGGAATCCGAGTGGCGGGCTCAAATCAGCT 404
D8	 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
OY	405 GAAGTGTTGTTGGCTCAACAGTGCTCTTAACAGTGCGGCAGGCGCTTTTGACGCTTG 464

Db 41 GluValValArgCysLeuSnsSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60  
QY 465 GAAAACTCCAGCTGTGACACAGATGGAGTATGACATCTGTAAATCCTTTGTACAGC 524  
Db 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80  
QY 525 GCTGCTAAATTGACACTCAGAGGAAAAGCATTCGTCAAGAGAGCTTAAATGATCAGCC 584  
Db 81 AlaAlaIlyPheAspThrGlnGlyLysAlaPheValGlyGlnSerLeuLysCysIleAla 100  
QY 585 AACGGGGTCACTCCCAAGCTCTTCTCGCATTCGAGAGTGTCTCCACTTTCCAAAGATG 644  
Db 101 AsnGlyValThrSerIySerValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120  
QY 645 ATTGCTGAGTGCAGAGAGAGTGTCTACAGAGCTGAATGTGTGACAGATCCGCAAGCGG 704  
Db 121 IleAlaGluValGlnGlnGlnCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140  
QY 705 AACCTGAAAGCCATCACTGAGTGTCTCAAGCTGCCCAATCACTTCCAAAGATACTAT 764  
Db 141 AsnProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160  
QY 765 AACAGACTTGTCCGAGAGCTGTGATGTGATGAAAGACAGCTCAGACATCAGAGAC 824  
Db 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGlnAspThrValSerThrIleArgAsp 180  
QY 825 AGCCTGATGAGAGAAATTTGGGCTTAACATGAGCAGAGCTTCCACATCCTGACAGACAG 884  
Db 181 SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200  
QY 885 CACTGTGCCCAACACACACCCAGAGCTGACTTCAACAGAGAGCAGCCATGAGCCGACG 944  
Db 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlnProGln 220  
QY 945 AAGCTGAAAGTCCCTCCTCAGGAACCTCCGAGGTGAGAGAGAGCTCCCTCCCAATCAAA 1004  
Db 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGlnAspSerProSerHisIleLys 240  
QY 1005 CGCAGATCCCATGAGAGTGCA 1025  
Db 241 ArgThrSerHisGlnSerAla 247  
RESULT 8  
ID AAB62690 standard; protein; 247 AA.  
XX  
AC AAB62690;  
XX  
DT 06-AUG-2001 (first entry)  
XX  
DE Lng108, a diagnostic marker for cancer.  
XX  
KW Lng108; cancer; diagnostic marker; cytotoxic; immune response; imaging.  
XX  
OS Homo sapiens.  
XX  
PN MO200132209-A1.  
XX  
PD 10-MAY-2001.  
XX  
PF 03-NOV-2000; 2000MO-US030482.  
XX  
PR 04-NOV-1999; 99US-0163444P.  
XX  
PA (DIAD-) DIADEXUS INC.  
XX  
PI Recipon H, Macina RA, Chen S, Sun Y;  
XX  
DR WPI; 2001-316366/33.  
XX  
DR N-PSDB; AAF83823.  
PT Novel assay for diagnosing and monitoring cancer, involves determining

PT levels of Lng108 in cells, tissues or bodily fluids of the patient, and  
PT comparing with control.  
XX  
PS Disclosure; Page 33-34; 36pp; English.  
XX  
CC The invention relates to diagnosing the presence of cancer or diagnosing  
CC metastases of cancer in a patient that involves determining levels of  
CC Lng108 in a sample of cells, tissues or bodily fluids in a patient, and  
CC comparing the determined levels with levels of Lng108 in a normal human  
CC control. The method is useful for diagnosing the presence of cancer,  
CC diagnosing metastases of cancer, staging cancer, monitoring cancer, and  
CC monitoring a change in stage of the cancer in a patient. A therapeutic  
CC agent which is an antibody labeled with paramagnetic ions or a  
CC radioisotope, and conjugated with a cytotoxic agent is useful for imaging  
CC cancer in a patient. A molecule which downregulates the expression or  
CC activity of Lng108, is useful for treating cancer in a patient. Lng108  
CC protein is useful for inducing an immune response against a target cell  
CC expressing Lng108. The present sequence represents the human Lng108  
CC polypeptide  
CC  
SQ Sequence 247 AA:  
XX  
XX  
Alignment Scores:  
Pred. No.: 6,45e-115 Length: 247  
Score: 1268.00 Matches: 247  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 18.56% Indels: 0  
DB: 4 Gaps: 0  
US-09-703-350B-75 (1-3900) x AAB62690 (1-247)  
QY 285 ATGCTCCAAAATCAGACAGTCTTCTGTGCTGTGATATCACTGCTTCTGCAACCCATGAG 344  
Db 1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGln 20  
QY 345 GGGAGAGAGATGATGCTGTGAGCCCGAGAAATCCCGAGTGGGGCTCAAAATCAGCT 404  
Db 21 AlaGlnGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40  
QY 405 GAAGTGTCTGTTGCTTCAACAGTCTCTTACAGGTGGCTGGGGGCTTTTGATGCTGTG 464  
Db 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60  
QY 465 GAAAACTCCAGCTGTGACACAGATGGAGTATGACATCTGTAAATCCTTTGTACAGC 524  
Db 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80  
QY 525 GCTGCTAAATTGACACTCAGAGGAAAAGCATTCGTCAAGAGAGCTTAAATGATCAGCC 584  
Db 81 AlaAlaIlyPheAspThrGlnGlyLysAlaPheValGlyGlnSerLeuLysCysIleAla 100  
QY 585 AACGGGGTCACTCCCAAGCTCTTCTCGCATTCGAGAGTGTCTCCACTTTCCAAAGATG 644  
Db 101 AsnGlyValThrSerIySerValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120  
QY 645 ATTGCTGAGTGCAGAGAGAGTGTCTACAGAGCTGAATGTGTGACAGATCCGCAAGCGG 704  
Db 121 IleAlaGluValGlnGlnGlnCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140  
QY 705 AACCTGAAAGCCATCACTGAGTGTCTCAAGCTGCCCAATCACTTCCAAAGATACTAT 764  
Db 141 AsnProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160  
QY 765 AACAGACTTGTCCGAGAGCTGTGATGTGATGAAAGACAGCTCAGACATCAGAGAC 824  
Db 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGlnAspThrValSerThrIleArgAsp 180  
QY 825 AGCCTGATGAGAGAAATTTGGGCTTAACATGAGCAGAGCTTCCACATCCTGACAGACAG 884  
Db 181 SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200  
QY 885 CACTGTGCCCAACACACCCAGAGCTGACTTCAACAGAGAGCAGCCATGAGCCGACG 944

Db	201	HicScyAlaGlnIthrHisProArgAlaAspPheMetArgArgIThrAsnGluProGln	220
Qy	945	AAAGTAAAGTCCTCCTCGAGAACTCCGAGGTGAGAGACCTCCCTCCCAATCAA	1000
Db	221	LyLeuLysValLeuLeuArgAsnMetArgGlyGluGlnAspSerProSerHisIleLys	240
Qy	1005	CGACATCCCATGAGAGTGA	1025
Db	241	ArgThrSerHisLeuSerIle	247

## RESULT 9

ID	AB06259	standard; protein; 247 AA.
XX		
XX	AB06259;	
XX		
XX	23-MAY-2002	(first entry)
DT		
XX		
XX		
D5		Human stanoicocalcin 1 protein.
XX		
KW	Human; stanoicocalcin 1; osteoparhic; osteogenesis failure; osteoporosis;	
KW	bone mass reduction; traumatic bone injury; osteomalacia; bone disease;	
KW	rheumatic bone disease; cancer associated bone disease; rachitis;	
KW	arthritis deformans.	
KW		

PI Yoshiko Y, Koide Y, Igarashi A, Takano S, Maeda N, Audin JE,  
XX  
WPI: 2002-164600/21.  
DR  
N-PSDB; ABL40225.

PT Agent used for treating bone diseases, e.g. osteoporosis, traumatic bone  
 PT injury, osteomalacia, rheumatic bone diseases, bone diseases associated  
 PT with cancer and arthritis deformans containing strontiumcalcium I.  
 XX  
 Claim 2, Fig 1, 24pp; Japanese.

CC The present invention describes an agent containing stanoicalcin 1,  
CC particularly of human origin. Stanoicalcin 1 has osteoprotic activity.  
CC The agent can be used for treating diseases relating to osteogenesis  
CC failure or reduction in bone mass e.g. osteoporosis, traumatic bone  
CC injury, osteomalacia, rheumatic bone diseases, bone diseases associated  
CC with cancer, bone diseases due to phosphorus or calcium metabolic error  
CC rachitis and arthritis deformans. The agent increases bone mass. The  
CC present sequence represents human stanoicalcin 1

## SQ Sequence 247 AA;

Alignment Scores:	
Pred. No.:	6,45e-115
Percent Similarity:	1268.00
Score:	100.00%
Best Local Similarity:	100.00%
Query Match:	18.56%
DB:	5
Length:	247
Matches:	247
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-703-350B-75 (1-3900) X ABB06259 (1-247)

Qy 285 ATGCTCCAAAACCTCAGCAGTGGTCTTGCTGGTATCAGTGGCTTTCGCAACCCCATGAG 344  
Db 1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisLeu 20

QY	345	GGGAGAGAGATGACTCTGTGTAGAGCCCAAGAAATCCGAGTGGGGGCTCAAACTCAGCT	404
Db	21	AlaIugInhmsabpSerValSerProArglySerArgValAlaAlaGlnhmsSerIa	40
QY	405	GAACTGTGTCCTTCCCTCCACAGTGCCTCTACAGGTGGCTGGGCGGCTTTTGATGCTGTG	464
Db	41	GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu	60
QY	465	GAAATCCCACTGCTGTGACACAGATGGGATGTATGATACCTGTAAATCCTTGTGACAGC	524
Db	61	GlnAsnSerThrCysAspThrAspGlyMetCylMetCylSerPheLeuTyrSerPheLeuTyrSer	80
QY	525	GCTCTAAATTGTGACACTCAGAGGAAAGACATTCGTCAAGAAGACTTTAAATGCATGCGC	584
Db	81	AlaAlaTyrPheAspThrGlnGlnGlyLeuAlaPheValIysGlnSerLeuTyrCysIleAla	100
QY	585	AACGGGGTCACTCTCCAAAGTCTTCTCTGGCCATTGGAGAGTGTCTCACTTCCAAAGATG	644
Db	101	AsnGlyValThrSerIysValPheLeuAlaIleArgArgCysSerThrPheGlnThrMet	120
QY	645	ATTGCTGAGGTGACGAAAGAGTGTGTACAGCAGCTGTGATGTGTGTCAGCATGCGCAAGCG	704
Db	121	IleIleGlnValGlnGlnGlnCysTyrSerIysLeuAsnValCysSerIleAlaTyrArg	140
QY	705	AACCTTGAAAGCATCACTGAGAGTGTGTCCAGTGGCCCATCACTTCTCCAAAGATACAT	764
Db	141	AsnProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr	160
QY	765	AACAGACTTGGCCAGAGCGTCTGGAATGTATGAAGACACAGTCAGACACATGAGAGAC	824
Db	161	AsnArgLeuValArgSerLeuLeuGlnCysAspGlnAspThrValSerThrIleArgAsp	180
QY	825	AGCTGTATGAGAAATATTGGGCTTAACTAGTGGCCAGGCTCTTCCACATCTGTGCAAGACAG	884
Db	181	SerLeuMetGlnTyrIleGlyProAsnMetAlaSerLeuProThrIleLeuGlnThrAsp	200
QY	885	CACGTGTGCCCAACACACCCAGAGCTGACTTCAACAGAGACCCACCAATGAGCCGAG	944
Db	201	HisCysAlaGlnThrHisProArgAlaAspPheAsnArgAlaGlnThrAsnGlnProGln	220
QY	945	AAGCTGAAAGTCTCTCTCAGGAACTTCGAGGTGAGAGACTCTCCTCCCAATCAA	1004
Db	221	LysLeuTyrValLeuLeuArgAsnLeuArgGlyGlnGlnAspSerProSerHisIleLys	240
QY	1005	CGCACATCCCATGAGATGCA	1025
Db	241	ArgThrSerHisGlnSerIa	247

RESULT 10

ID	ABP97748	standard; protein; 247	AA
XX			
AC	ABP97748;		
XX			
DT	28-MAY-2003	(first entry)	

DE Amino acid sequence of human STC1 polypeptide.

KM Human, angiogenesis; wound healing; retinopathy; ischemia; inflammation;  
KM microvasculopathy; bone healing; skin inflammation; HOG3; HOG6; HOG18;  
KM follicular development; CA9; HXB, IGFBP5; HPRAP; STC1; mlg-6; SSR4;  
KM cancer.

OS	Homo sapiens.
XX	
PN	W02003010205-A1.
XX	
PD	06-FEB-2003.

PF	26-JUL-2002; 2002WO-US023786.
XX	
PR	26-JUL-2001; 2001US-0307600P.

PR	24-JUL-2002; 2002US-00201642.
XX	
PA	(UYDU-) UNIV DUKE MEDICAL CENT.
PI	
PI	Riggins CJ, Lal A;
XX	
DR	WPI; 2003-239423/23.
XX	
DR	N-PSDB; ABZ77288.
XX	
PT	Inhibiting angiogenesis for treating wound healing, retinopathy,
PT	ischemia, inflammation, microvasculopathy, bone healing, skin
PT	inflammation or follicular development by providing to a subject an
PT	antisense polynucleotide.
XX	
PS	Claim 4; Page 61; 66pp; English.
XX	
CC	The present sequence is a human STC1 polypeptide. It is used in the
CC	method of the invention. The specification describes a method modulating
CC	angiogenesis associated with wound healing, retinopathy, ischemia,
CC	inflammation, microvasculopathy, bone healing, skin inflammation or
CC	follicular development. The method comprises providing to a subject HOG3,
CC	HOG8, HOG18, CA9, HXB, IGFBB5, HPARP, STC1, miG-6 or SSR4. The methods
CC	antisense polynucleotides, polypeptides and antibodies are useful for
CC	treating wound healing, retinopathy, ischemia, inflammation,
CC	microvasculopathy, bone healing, skin inflammation or follicular
CC	development, or cancer such as breast, colon or lung cancer, or
CC	glioblastoma
CC	
XX	
SO	Sequence 247 AA;
Alignment Scores:	
Pred. No.:	6,45e-115 Length: 247
Score:	1268.00 Matches: 247
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	18.56% Indels: 0
DB:	6 Gaps: 0
US-09-703-350B-75 (1-3900) x ABP97748 (1-247)	
QY	285 ATGCTCCAAACTCAGACAGTGTCTTGCGTGTGATCAGTGCCTTCGCAACCATGAG 344
Db	1 MelLeuGlnAsnSerIaValLeuIeuValIeSerAlaSerAlaThrIsglu 20
QY	345 GCGGAGCAGATGACTCTGTGAGCCCGAGAAATCCGAGTGGCGGCTCAAAATCAGCT 404
Db	21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
QY	405 GAAGTGGTTTCGCTTCAACAGTGTCTACAGAGTGGCGTGGCGGGGCTTTGGATGGCTG 464
Db	41 GluValValArgGlyGlyLeuAsnSerAlaLeuGlnValGlyGlyAlaPheAlaCysLeu 60
QY	465 GAAAACTCCACTGTGACACAGATGGGATGTATGACATCTGTAATCCTTTGTACAGC 524
Db	61 GluAsnSerThrCysAspThrAspGlyMetIleAspIleCysLysSerPheLeuTyrSer 80
QY	525 GCGCTAAATTGGACACTCAGGGAAGAAAGCATTCGTCAAGAAGAGAGTTAAATGATGCC 584
Db	81 AlaAlaLysPheAspThrGlnGlnGlyAlaPheValLysGluSerLeuLysCysIleAla 100
QY	585 AACGGGGTCACTCCCAAGGCTCTTCCTCGGCATTCGGAAGTGTCTCCACTTCCAAAGATG 644
Db	101 AsnGluValThrSerLysValPheLeuAlaIleArgGlyCysSerThrPheGlnArgMet 120
QY	645 ATTGCTGAGGTGCAGAGAAAGTGCTACAGCAAGCTGAATGTGTGCAGATGGCCAAACGG 704
Db	121 IleAlaGluValGlnGlnGlnGlyCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
QY	705 AACCTCGAAGCCATCACTGAGGTGCGCCAGCTGCCCAATCACTTCCACAGATATCAT 764
Db	141 AsnProGlnAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
QY	765 AACGACTTGTCCGAAGCCTGCTGGAATGTATGAAGACACAGTCAAGCATATGAGAC 824

Db	161	AsnArgLeuValArgSerLeuLeuGluLysaspIuAspThrValSerThrIleArgAsp	180
Qy	825	AGCCTGATGGAGAAATTTGGGCTTAACTGGCCAGCCTCTTCCACATCTGCAGACAGAC	884
Db	181	SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp	200
Qy	885	CAGTGAGCCCAAAACACCCACGAGCTACTACTTCAACAGGAGACCCACCATGAGCCGAG	944
Db	201	HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgGlnIleProGln	220
Qy	945	AAGCTGAAAGTCTCTCTCAGACACCTCGAGGTAGGAGAGACTCTCCCTCCACATCAA	1000
Db	221	LysLeuLysValLeuLeuArgAsnLeuArgIlyLugLusPserProSerHisIleLys	240
Qy	1005	CGCAGATCCCATGAGAGTCA	1025
Db	241	ArgThrSerHisGluSerAla	247
RESULT 11			
AC	ABR47600	standard; protein; 247 AA.	
AC	ABR47600;		
DT	12-JUN-2003	(first entry)	
DE	Breast cancer associated protein sequence SEQ ID NO:441.		
XX	Human, breast cancer; cytostatic; gene therapy.		
OS	Homo sapiens.		
XX	WO2003004989-A2.		
PN	16-JAN-2003.		
PD			
XX			
PF	21-JUN-2002; 2002WO-US019669.		
XX			
PR	21-JUN-2001; 2001US-0299887P.		
PR	27-JUN-2001; 2001US-0301572P.		
PR	18-JUL-2001; 2001US-0306501P.		
PR	25-SEP-2001; 2001US-0325002P.		
PR	05-MAR-2002; 2002US-0362585P.		
PR	14-MAY-2002; 2002US-0380391P.		
XX			
PA	(MILL-) MILLENIUM PHARM INC.		
XX			
PI	Lillie J, Ganavavaru M, Glatt K, Hoerish S, Kamatkar S;		
PI	Mertens M, Monahan JE, Wyer V, Wang Y, Xu Y, Zhao X, Meyers RE;		
PI	Bast RC, Horrobasyi GN, Fuzstai L, Meric F, Sahin A, Mills GB;		
XX			
XX	WPI; 2003-210381/20.		
DR	N-PSDB; ACC50301.		
PT	Breast cancer diagnosis or treatment by comparing the level of expression		
PT	of a marker in a patient sample with that in the control non-breast		
PT	cancer sample.		
XX			
PS	Claim 1; SEQ ID NO 441; 128BP; English.		
XX			
CC	The present invention describes a method for assessing whether a patient		
CC	is afflicted with breast cancer. The method comprises comparing the level		
CC	of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and		
CC	ABR47386 to ABR4732) in a patient sample and the normal level of		
CC	expression of the marker in a control non-breast cancer sample, where a		
CC	significant increase in the level of expression of the marker in the		
CC	patient sample and the normal level is an indication that the patient is		
CC	afflicted with breast cancer. The breast cancer associated sequences from		
CC	the present invention have cytostatic activities and can be used in gene		
CC	therapy. The method is useful for diagnosing and treating breast cancer.		
CC	N.B. The sequence data for this patent did not form part of the printed		
CC	specification, but was obtained in electronic format directly from WIPO		



QY 405 GAAGTGTTCCTGCTCAACAGTCTCTACAGTTCGCTCGGGGCTTTTGATCTCTG 464  
 DB 41 GluValValArgCysLeuSnsSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60  
 QY 465 GAAATCTCCAGCTGTGACAGATGGAGATGATGATCATCTGTAATCTTCTGTGACAG 524  
 DB 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLeuSerPheLeuTyrSer 80  
 QY 525 GCTGCTAAATTTGACACTCAGGAGAAAGCATTCGTCAAAAGAGACTTAATGATCGCC 584  
 DB 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValIleGlnSerLeuLysCysIleAla 100  
 QY 585 AAGGGGGTCACTCCCAAGCTTCCTCGCATTCGAGAGTGGCTCCACTTCCAAAGAGAG 644  
 DB 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120  
 QY 645 ATGCTGAGGTGAGAGAGAGTGTCTACAGCACTGATGTGACAGCATCCGCAAGCG 704  
 DB 121 IleAlaGlnValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 140  
 QY 705 AACCTGAAAGCTCTCACTGAGGTCTCTCAGCTGCCAATACCTTCTCCAAAGATCTAT 764  
 DB 141 AspProGlnAlaIleThrGlnValAlaGlnLeuProAsnHisPheSerAsnArgTyrTyr 160  
 QY 765 AACGACTTGTCCGAAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 824  
 DB 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGlnAspGlnAspGlnAspGlnAspGln 180  
 QY 825 AGCTGTGAGAGAAATTTGGGCTTACATGAGCAGCTCTTCCACATCTCTGACAGACAG 884  
 DB 181 SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200  
 QY 885 CACTGTGCCCCAACAACACACCCAGAGCTGATTCATCAAGAGAGAGAGAGAGAGAGAG 944  
 DB 201 HisCysLeuGlnThrHisProArgAlaAspPheAsnArgArgThrGlnGlnGlnGlnGln 220  
 QY 945 AAGCTGAAATCTCTCTCCTCAGAACTTCGAGTGTGAGAGAGAGACTCTCTCCACATCAA 1004  
 DB 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGlnAspSerProSerHisIleLys 240  
 QY 1005 CGCACATCCCATGAGAGTGCA 1025  
 DB 241 ArgThrSerHisGlnSerAla 247  
 RESULT 13  
 ADD48082  
 ID ADD48082 standard; protein; 247 AA.  
 AC ADD48082;  
 XX 29-JAN-2004 (first entry)  
 DE Human Protein P52823, SEQ ID NO 13779.  
 XX Human; pain; neuronal tissue; gene therapy;  
 KW spinal segmental nerve injury; chronic constriction injury; CCI;  
 KW spared nerve injury; SNI; Chung.  
 XX Homo sapiens.  
 OS  
 PN WO2003016475-A2.  
 XX 27-FEB-2003.  
 PF 14-AUG-2002; 2002WO-US025765.  
 PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX

PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX WPI; 2003-268312/26.  
 DR GENBANK; P52823.  
 XX New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX  
 PS Claim 1; Page; 1017pp; English.  
 XX  
 XX The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide; a host cell  
 CC comprising the vector; a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a human protein (shown in table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 247 AA;  
 Alignment Scores:  
 Pred. No.: 6,45e-115 Length: 247  
 Score: 1268.00 Matches: 247  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 18.56% Indels: 0  
 DB: Gaps: 0  
 US-09-703-350B-75 (1-3900) x ADD48082 (1-247)  
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 DB 1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisIle 20  
 QY 345 GCGGAGCAGATGATCTGTGAGCCCGGAAATCCGAGAGGGGGCTCAAAATCTCAGCT 404  
 DB 21 AlaGlnGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40  
 QY 405 GAAGTGTTCCTGCTCAACAGTCTCTACAGTTCGCTCGGGGCTTTTGATGCTCTG 464  
 DB 41 GluValValArgCysLeuSnsSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60  
 QY 465 GAAATCTCCAGCTGTGACAGATGGAGATGATGATCATCTGTAATCTTCTGTGACAG 524  
 DB 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLeuSerPheLeuTyrSer 80  
 QY 525 GCTGCTAAATTTGACACTCAGGAGAAAGCATTCGTCAAAAGAGACTTAATGATCGCC 584  
 DB 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValIleGlnSerLeuLysCysIleAla 100  
 QY 585 AAGGGGGTCACTCCCAAGCTTCCTCGCATTCGAGAGTGGCTCCACTTCCAAAGAGAG 644  
 DB 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120







AC AB084399;  
XX  
DT 29-UTL-2004 (first entry)  
XX  
DE Human stanniocalcin protein.  
XX  
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KW surfactant depletion; anti-allergic; anti-inflammatory; antispasmodic;  
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KW pulmonary transplantation rejection.  
XX  
OS Homo sapiens.  
XX  
PN WO200285309-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013143.  
XX  
PR 24-APR-2001; 2001US-0286036P.  
XX  
PA (EPIC-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR MPI; 2003-093058/08.  
DR N-PSDB; ABD20997.  
XX  
PT Pharmacological composition for treating asthma, has antisense  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
XX  
PS Claim 15; SEQ ID NO 6; 763bp; English.  
XX  
CC This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has anti-allergic, anti-inflammatory, antispasmodic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX  
SQ Sequence 247 AA;

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Best Local Similarity:	100.00%	Mismatches:	0
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DB:	7	Gaps:	0
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QY	345	GCGAGACAGATGACTCTGCTGAGCCCGACGAAATCCGAGGGCGGCTTAAATCAGCT	404
DB	21	AlaGlnGlnAAspSerValSerProArgLysSerArgValAlaAlaGlnAAsnSerAla	40
QY	405	GAAGTGTTCCTGCTTCCATCAAGTGTCTTACAGGTCTGCGGGCTTTTGCATGCTG	464
DB	41	GluValValArgCysLeuAAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu	60
QY	465	GAATCTCCACTCTGTGACACAGATGGATGTATGACATCTGTAATCTTCTTACAGC	524
DB	61	GluAsnSerThrCysAspThrAspGlyMetLysPheLysSerPheLeuLysSer	80
QY	525	GCTGCTAAATTTGACACTCAGGAGAAAGCATTCCTCAAGAGAGACTTAAATGATCGCC	584
DB	81	AlaAlaLysPheAspThrGlnGlnLysAlaPheValLysGlnSerLeuLysCysIleAla	100
QY	585	AACGGGGTACCTTCCAAAGTCTTCTTCTGCGCATTTGCGAGTCTTCTTCCAAAGATG	644
DB	101	AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet	120
QY	645	ATTGCTGAGTGCAGGAGAGATGCTTACAGCAAGTGTATGTGTCAGATCGCCAGCGG	704
DB	121	IleAlaGluValGlnGlnGluCysLysSerLysLeuAsnValCysSerIleAlaLysArg	140
QY	705	AACCTGAAAGCCATCTACTAGAGTGTCTCCAGCTGCCAATCTTCTTCCAAAGATCTAT	764
DB	141	AsnProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr	160
QY	765	AACGACTTGTCCGAAAGCTGTGTAATGTGATAAAGCAGTCAGACATGACAGAC	824
DB	161	AsnArgLeuValArgSerLeuLeuGlnCysAspGlnLysPheValSerThrIleArgAsp	180
QY	825	AGCTGATGAGAAATTTGGCTTACATGCGCAGCTCTTCCATCTCTGACAGAC	884
DB	181	SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp	200
QY	885	CATGTGCGCCAAACACACACCGACGCTGACTTTCACAGGAAACGACCAAGACCCGCG	944
DB	201	HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgValAsnGlnProGln	220
QY	945	AAGCTGAAAGTCCCTCCAGAGACCTCGAGGTAGAGAGACTCTCCCTCCACATGAAA	1004
DB	221	LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGlnLysSerProSerHisIleLys	240
QY	1005	CGACATCTCCATGAGAGTGCA	1025
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GenCore version 5.1.6  
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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	1268	18.6	247	2	US-09-038-597A-2
3	1268	18.6	247	2	US-08-460-529B-10
4	1268	18.6	247	2	US-08-431-117A-2
5	1268	18.6	247	4	US-09-361-736B-10
6	660.5	9.7	204	2	US-08-208-005C-5
7	660.5	9.7	204	2	US-09-038-597A-5
8	628	9.2	170	4	US-08-460-529B-9
9	628	9.2	170	4	US-09-361-736B-9
10	362	5.3	302	3	US-08-831-132-2
11	362	5.3	302	3	US-09-416-150-2
12	362	5.3	302	4	US-09-193-881-23

13	362	5.3	302	4	US-09-361-736B-12	Sequence 12, Appl
14	356.5	5.2	251	4	US-09-361-736B-2	Sequence 2, Appl
15	356	5.2	296	3	US-08-831-132-14	Sequence 14, Appl
16	356	5.2	296	3	US-09-416-150-14	Sequence 14, Appl
17	338.5	5.0	251	2	US-08-460-529B-2	Sequence 2, Appl
18	183	2.6	362	1	US-08-415-751-6	Sequence 6, Appl
19	175	2.5	362	1	US-08-415-751-35	Sequence 35, Appl
20	163	2.3	2211	3	US-09-738-884-1	Sequence 1, Appl
21	163	2.3	2211	4	US-10-056-961A-1	Sequence 1, Appl
22	157.5	2.3	539	4	US-09-538-092-160	Sequence 160, App
23	149	2.1	1400	3	US-08-630-915A-37	Sequence 37, Appl
24	149	2.1	1400	4	US-09-879-957-37	Sequence 37, Appl
25	148.5	2.2	215	4	US-09-248-796A-22017	Sequence 21017, A
26	148.5	2.2	2732	4	US-09-086-436-30	Sequence 30, Appl
27	147.5	2.1	1345	2	US-08-977-767-3	Sequence 3, Appl
28	146.5	2.1	109	2	US-08-527-044-2	Sequence 2, Appl
29	146.5	2.1	109	3	US-09-013-780-2	Sequence 2, Appl
30	146.5	2.1	910	4	US-08-997-685A-2	Sequence 2, Appl
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32	143.5	2.1	339	4	US-09-324-258-2	Sequence 2, Appl
33	143.5	2.1	339	4	US-09-358-092-964	Sequence 54, App
34	143.5	2.1	345	4	US-09-324-258-15	Sequence 15, Appl
35	143.5	2.1	379	4	US-09-248-796A-23759	Sequence 23759, A
36	143	2.0	1417	3	US-08-900-230-3	Sequence 42577, A
37	141	2.1	622	4	US-09-491-356C-9	Sequence 9, Appl
38	140	2.0	2074	4	US-09-338-092-1171	Sequence 1171, Ap
39	139	2.0	1586	4	US-09-421-356C-8	Sequence 8, Appl
40	139	2.0	2023	4	US-09-421-356C-8	Sequence 1377, Ap
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43	136.5	2.0	1319	4	US-09-538-092-1291	Sequence 29, Appl
44	135	2.0	428	1	US-08-190-802A-29	Sequence 29, Appl
45	135	2.0	428	3	US-08-477-346-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1  
US-08-208-005C-2  
; Sequence 2, Application US/08208005C  
; Patent No. 5837498  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Corpucles of Stannius Protein, Stanniolocalcin  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER PARK ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/208, 005C  
; FILING DATE: 8 MARCH 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 345800-78  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 2:



```

Db      101  AaaglyValThrSerIysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
QY      645  ATTGCTGAGTGCAGAGAAAGTGTCTACAGCAAGCTGAATGTGTGAGCATCGCCAAAGCG 704
Db      121  IleAlaGluValGlnGluGluCysIysIysSerIysLeuAsnValCysSerIleAlaIysArg 140
QY      705  AACCTGAAAGCCATCATCTAGAGGTCTCCAGCTGCCCATCTTTCTCCAAAGATATCTAT 764
Db      141  AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyr 160
QY      765  AACAGACTGTGTCGAGAGCTGTGGATGTGATGAAGACAGCAGTACAGCAATCAGAGAC 824
Db      161  AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
QY      825  AGCCTGATGAGAGAAAATTGGGCTTAACATGGCCAGCTCTTCCACATCTCTGACAGAC 884
Db      181  SerLeuMetGluIysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
QY      885  CACTGTGCCCCAAACACACCCAGAGCTGACTTCACAGAGAGAGACCAATGAGCGGAG 944
Db      201  HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
QY      945  AAGCTGAAGTCTCTCTCCAGAACTCCGAGGTGAGAGAGACTCTCCCTCCCAATCAAA 1004
Db      221  LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
QY      1005  CGCACATCCCATGAGAGTGCA 1025
Db      241  ArgThrSerHisGluSerAla 247

RESULT 3
US-08-460-529B-10
/ Sequence 10, Application US/08460529B
/ Patent No. 5994103
/ GENERAL INFORMATION:
/ APPLICANT: OLSEN, ET AL.
/ TITLE OF INVENTION: Human Stanniocalcin-alpha
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: CARELLA, BYRNE, BAIR, GILFILLAN,
/ ADDRESSEE: CECCHI, STEWART & OLSTEIN
/ STREET: 6 BECKER FARM ROAD
/ CITY: ROSELAND
/ STATE: NEW JERSEY
/ COUNTRY: USA
/ ZIP: 07068
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 INCH DISKETTE
/ COMPUTER: IBM PS/2
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: WORD PERFECT 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/460,529B
/ FILING DATE: June 2, 1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US94/13206
/ FILING DATE: 10 NOV 1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MULLINS, J.G.
/ REGISTRATION NUMBER: 33,073
/ REFERENCE/DOCKET NUMBER: 325800-334 (PFI43)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-994-1744
/ TELEFAX: 201-994-1744
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 247 AMINO ACIDS
/ TYPE: AMINO ACID
/ STRANDEDNESS:
/ TOPOLOGY: LINEAR
/ MOLECULE TYPE: PROTEIN

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US-08-460-529B-10
Alignment Scores:
Pred. No.: 9,296-121
Score: 1268.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 18.56%
Db: 2
Gaps: 0

US-09-703-350b-75 (1-3900) x US-08-460-529B-10 (1-247)
QY      285  ATGTCCAAACTCAGAGAGTCTTGTGCTGTGATGATCATGCTTCTTGCAACCCATGAG 344
Db      1  MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
QY      345  GCGAGAGAGATGACTCTGTGAGCCGCCAGAAATCCCGAGTGGCGCTCAAACTCAGCT 404
Db      21  AlaGluGlnAsnSpsSerValSerProArgLysSerArgValAlaIleGlnAsnSerAla 40
QY      405  GAACTGTTGTTGCTCCCAACAGTCTCTACAGGTGAGTGGCGGCGCTTGTGATGCTG 464
Db      41  GluValValArgCysLeuAsnSerAlaLeuGlnValIleCysGlyAlaPheHisCysLeu 60
QY      465  GAAACTCCACTGTGACACAGATGGATGTATGACATCTGTAAATCTTCTTGATCAGC 524
Db      61  GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
QY      525  CCTGCTAAATTGACACTCAGGAGAAAGCATTCGTCAAGAGAGCTTAAATGATGATGCC 584
Db      81  AlaIleLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
QY      585  AAGGAGGTGACCTCCAGAGTCTTCTCGCCATTCGAGTGTGAGTGTCTCACTTCCAAAGATG 644
Db      101  AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
QY      645  ATTGCTGAGTGCAGAGAAAGTGTCTACAGCAAGCTGAATGTGTGACATCGCCAAAGCG 704
Db      121  IleAlaGluValGlnGluGluCysIysSerLysLeuAsnValCysSerIleAlaIysArg 140
QY      705  AACCTGAGGCCATCATCTGAGGTGCTGACAGTGTGCCCATCTCTCCCAATCAATCTAT 764
Db      141  AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyr 160
QY      765  AACAGACTTGTCCAGAGCTCTGGAATGTGATGAAGACAGTACAGCAATCAGAGAC 824
Db      161  AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
QY      825  AGCCTGATGAGAGAAAATTGGGCTTAACATGGCCAGCTCTTCCACATCTGACAGAC 884
Db      181  SerLeuMetGluIysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
QY      885  CACTGTGCCCCAAACACACCCAGAGCTGACTTCACAGAGAGACCAATGAGAGCGGAG 944
Db      201  HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
QY      945  AAGCTGAAGTCTCTCTCCAGAACTCCGAGGTGAGAGAGACTCTCCCTCCCAATCAAA 1004
Db      221  LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
QY      1005  CGCACATCCCATGAGAGTGCA 1025
Db      241  ArgThrSerHisGluSerAla 247

RESULT 4
US-08-431-117A-2
/ Sequence 2, Application US/08431117A
/ Patent No. 5994301
/ GENERAL INFORMATION:
/ APPLICANT: OLSEN, ET AL.
/ TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:

```

```

ADDRESS: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,117A
CLASSIFICATION: 435
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,005
FILING DATE: 8 MARCH 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-296
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-431-117A-2

Alignment Scores:
Pred. No.: 9,29e-121 Length: 247
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.56% Indels: 0
Gaps: 0
DB: 2

US-09-703-350B-75 (1-3900) x US-08-431-117A-2 (1-247)

QY 285 ATGCTCCAAATCTGACAGTCTTCTGCTGCTGATGATGATGCTTTCGCAACCCAGAG 344
DB 1 MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
QY 345 GCGGAGCAGAAATGACTGTGTGAGCCCGAGAAATCCCGAGTGGCGCTCAAAACTCAGCT 404
DB 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
QY 405 GAAGTGGTTCGTTGCTTCAACAGTGTCTTACAGTGGCTGGCGGGCTTTTGCATGCTG 464
DB 41 GluValAlaArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
QY 465 GAAATCTCACCTGATGACAGATGGATGTATGATCATGTGTAATCCCTCTTGACAGC 524
DB 61 GluAsnSerThrCysAspThrAspGlyMetCysGlySerPheLeuThrSer 80
QY 525 GCTGCTAAATTTGACACTGAGGAAAAGCATTGCTCAAGAGAGCTTAAATGCAATGCC 584
DB 81 AlaAlaIleValPheAspThrGlnGlyValAlaPheValIleGlnSerLeuIleCysIleAla 100
QY 585 AACGGGGTCACTCCAGAGCTTCTCTCGCATTCGAGAGTGTCCACTTCCAAAGAGATG 644
DB 101 AsnGlyValThrSerIleValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
QY 645 ATTGCTGAGTGCAGAGAGAGTGTACAGCAAGCTGAATGTGTGACAGCATGCCAGCGG 704
DB 121 IleAlaGluValGlnGlnGluCysIleSerIleAsnValCysSerIleAlaIleArg 140

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QY 705 AACCTGAGACATCACTGAGTGTGTGACAGTGGCCCACTTCTTCCAAACAGATACTAT 764
DB 141 AsnProGlnAlaIleThrGlnValGlnLeuProAsnHisPheSerAsnArgTyr 160
QY 765 AACGACTTGTCCGACCTGCTGGAATGTGATGAGACACACTGCAGCAATACAGAGAC 824
DB 161 AsnArgLeuValArgSerLeuLeuGluCysAspGlnAspThrValSerThrIleValAsp 180
QY 825 AGCTGATGAGAAAATTGGGCTTAACATGAGCCAGCCCTCTTCCACATCTGCAGAGAC 884
DB 181 SerLeuMetGluIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
QY 885 CACTGTGCCCAACACCCACGAGCTGATTTGAAACAGAGACGACCAATGAGCCGACG 944
DB 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlnProGln 220
QY 945 AAGCTGAAGTCCCTCCAGAAACCTCCGAGTGTGAGAGAGACCTCCCTCCACATCAAA 1004
DB 221 LysLeuIleValLeuLeuArgAsnLeuArgGlyGlnGlnAspSerProSerHisIleLys 240
QY 1005 CGCACATCCCATGAGAGTGA 1025
DB 241 ArgThrSerHisGlnSerAla 247

RESULT 5
US-09-361-736B-10
Sequence 10, Application US/09361736B
Patent No. 6613877
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human StaminalcIn-Alpha
FILE REFERENCE: P143P101
CURRENT APPLICATION NUMBER: US/09/361,736B
CURRENT FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 08/460,529
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: PCT/US94/13206
PRIOR FILING DATE: 1994-11-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 247
TYPE: PRT
ORGANISM: human
US-09-361-736B-10

Alignment Scores:
Pred. No.: 9,29e-121 Length: 247
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.56% Indels: 0
Gaps: 0
DB: 4

US-09-703-350B-75 (1-3900) x US-09-361-736B-10 (1-247)

QY 285 ATGCTCCAAATCTGACAGTCTTCTGCTGCTGATGATGATGCTTTCGCAACCCAGAG 344
DB 1 MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
QY 345 GCGGAGCAGAAATGACTGTGTGAGCCCGAGAAATCCCGAGTGGCGCTCAAAACTCAGCT 404
DB 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
QY 405 GAAGTGGTTCGTTGCTTCAACAGTGTCTTACAGTGGCTGGCGGGCTTTTGCATGCTG 464
DB 41 GluValAlaArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
QY 465 GAAATCTCACCTGATGACAGATGGATGTATGATCATGTGTAATCCCTCTTGACAGC 524
DB 61 GluAsnSerThrCysAspThrAspGlyMetCysGlySerPheLeuThrSer 80
QY 525 GCTGCTAAATTTGACACTGAGGAAAAGCATTGCTCAAGAGAGCTTAAATGCAATGCC 584

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Db      |||
81 AlaAlaIyPheAspThrGlnGlnIyLysAlaPheValIyGluSerLeuIyCysIleAla 100
QY      |||
585 AACGGGGTCACTCCAGAGTCTTCTCGCATTCGGAGGTGTCCACTTCCAAAGATG 644
Db      |||
101 AangIyValThrSerIyValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
QY      |||
645 ATTGCTGAGTGCAGAGAGAGTGTACACAGACAGTGAATGTGTGAGCATCGCCAGAGCG 704
Db      |||
121 ILeAlaGluValAlaGlnGluIyCysIySerIySLeuAsnValCysSerIleAlaIyArg 140
QY      |||
705 AACCTGTAAGCCATCATCTAGAGGTGCTGCAGCTGCCCAATCACTTCCACAGATCATAT 764
Db      |||
141 AsnProGluAlaIleThrGluValAlaGlnLeuProAsnHisPheSerAsnArgTyr 160
QY      |||
765 AACAGACTGTGCGAAGGCTGCGAATGTGATGAAGACAGACAGTGCAGCATCGAGAGC 824
Db      |||
161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
QY      |||
825 AGCTGATGAGAAATTTGAGCTTAACATGAGCCAGCTTTCACATCTCTGAGACAGAGC 884
Db      |||
181 SerLeuMetGluIySerIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
QY      |||
885 CACTGCGCCCAACACACACAGAGTGACTTCAACAGAGACGACCAATGAGCCGAG 944
Db      |||
201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlnProGln 220
QY      |||
945 AAGCTGAAGTCCCTCTCCAGAACTCCGAGGTGAGAGAGACTCTCCCTCCACATCAAA 1004
Db      |||
221 IySLeuIyValLeuLeuArgAsnLeuArgAlaGlyGluGluAspSerProSerHisIleIyS 240
QY      |||
1005 CGCAGATCCCATGAGTGCA 1025
Db      |||
241 ArgThrSerHisGluSerAla 247

RESULT 6
US-08-208-005C-5
/ Sequence 5, Application US/08208005C
/ Patent No. 5837498
/ GENERAL INFORMATION:
/ APPLICANT: OLSEN, ET AL.
/ TITLE OF INVENTION: Corpuscles of Stannius Protein, Stannocalcin
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
/ ADDRESSEE: CECCHI, STEWART & OLSTEIN
/ STREET: 6 BECKER FARM ROAD
/ CITY: ROSELAND
/ STATE: NEW JERSEY
/ COUNTRY: USA
/ ZIP: 07068
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 INCH DISKETTE
/ COMPUTER: IBM PS/2
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: WORD PERFECT 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/208, 005C
/ FILING DATE: 8 MARCH 1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: FERRARO, GREGORY D.
/ REGISTRATION NUMBER: 36,134
/ REFERENCE/DOCKET NUMBER: 325800-78
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-994-1700
/ TELEFAX: 201-994-1744
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 204 AMINO ACIDS

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/ TYPE: AMINO ACID
/ STRANDEDNESS:
/ TOPOLOGY: LINEAR
/ MOLECULE TYPE: PROTEIN
US-08-208-005C-5

Alignment Scores:
Pred. No.: 1,35e-58 Length: 204
Score: 660.50 Matches: 118
Percent Similarity: 80.41% Conservative: 38
Best Local Similarity: 60.82% Mismatches: 37
Query Match: 9.67% Indels: 1
DB: 2 Gaps: 1

US-09-703-350B-75 (1-3900) x US-08-208-005C-5 (1-204)
QY      |||
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Db      |||
12 LeuValIleuGlyThrAlaAlaThrPheAspThrAspProGluAla---SerProArg 30
QY      |||
375 AATCCCGAGTGGCGGCTCAAACTCAGCTGAAGTGTGCTGCTCAACACTGCTCTA 434
Db      |||
31 ArgAlaArgPheSerSerAsnSerProSerArgValAlaArgCysLeuAsnGlyAlaLeu 50
QY      |||
435 CAGGTGGGCTGGCGGGGCTTTGCAATGCTGGAACCTCCACTGTGACACAGATGGGATG 494
Db      |||
51 AlaValGlyCysGlyThrPheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMet 70
QY      |||
495 TATGACACTGTGAATCTCTTGTGACAGCGCTGCTAAATTTGACACTCAGAGAAAGCA 554
Db      |||
71 HisAspIleCysGlnLeuPhePheHisThrAlaAlaThrPheAsnThrGlnIyLysThr 90
QY      |||
555 TTGCTCAAGAGAGACTTAAATGATGATGCGCCACGCGGCTCACTCCAGAGTCTTCTGCC 614
Db      |||
91 PheValIySgluSerLeuArgCysIleAlaAsnGlyValThrSerIySValPheGlnThr 110
QY      |||
615 ATTGGAAGTGTCTCCACTTTCACAGATGATTTGCTGAGGTGACAGAGTGTCTACAGC 674
Db      |||
111 IleArgArgCysGlyValPheGlnArgMetIleSerGluValGlnGluIyCysTyrSer 130
QY      |||
675 AAGCTGAATGTGTGACAGATGCGCCAGCGGAACCTGAAAGCATCACTGAGGTGTCCAG 734
Db      |||
131 ArgLeuAspIleCysGlyValAlaIyArgSerAsnProGluAlaIleGlyIyValIyAlaGln 150
QY      |||
735 CTGCCCCATCACTTCTCCACAGATGATTAACAGACTGTGCGAGCTGCGAATGT 794
Db      |||
151 ValProAlaHisPheProAsnArgTyrIySerThrLeuGluGlnSerLeuLeuAlaCys 170
QY      |||
795 GATGAGACACAGTGCAGACATGACAGACAGACCTGTGAGAAATTTGGCGCTACATG 854
Db      |||
171 AspGluGluThrValAlaValIyAlaValArgAlaGlyLeuValAlaIyGluGlyProAspMet 190
QY      |||
855 GCCAGCTCTTCCACATCTCTGACAGACAGACCTGTGCGCCA 896
Db      |||
191 GluThrLeuPheGlnLeuLeuGluIyAsnIyHisCysProGln 204

RESULT 7
US-09-038-597A-5
/ Sequence 5, Application US/09038597A
/ Patent No. 587280
/ GENERAL INFORMATION:
/ APPLICANT: OLSEN, ET AL.
/ TITLE OF INVENTION: Corpuscles of Stannius Protein,
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
/ ADDRESSEE: CECCHI, STEWART & OLSTEIN
/ STREET: 6 BECKER FARM ROAD
/ CITY: ROSELAND
/ STATE: NEW JERSEY
/ COUNTRY: USA
/ ZIP: 07068

```

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1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: 3.5 INCH DISKETTE
3 COMPUTER: IBM PS/2
4 OPERATING SYSTEM: MS-DOS
5 SOFTWARE: WORD PERFECT 5.1
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/09/038,597A
8 FILING DATE:
9 CLASSIFICATION:
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: 08/208,005
12 FILING DATE: 8-MARCH-1994
13 ATTORNEY/AGENT INFORMATION:
14 NAME: FERRARO, GREGORY D.
15 REGISTRATION NUMBER: 36,134
16 REFERENCE/DOCKET NUMBER: 325800-78
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: 201-994-1700
19 TELEFAX: 201-994-1744
20 INFORMATION FOR SEQ ID NO: 5:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 204 AMINO ACIDS
23 TYPE: AMINO ACID
24 STRANDEDNESS:
25 TOPOLOGY: LINEAR
26 MOLECULE TYPE: PROTEIN
27 US-09-038-597A-5
28
29 Alignment Scores:
30 Pared No.: 1,35e-58 Length: 204
31 Score: 660.50 Matches: 118
32 Percent Similarity: 80.41% Conservative: 38
33 Best Local Similarity: 60.82% Mismatches: 37
34 Query Match: Indels: 1
35 DB: Gaps: 2
36
37 US-09-703-350B-75 (1-3900) x US-09-038-597A-5 (1-204)
38
39 QY 315 CTGCTGATCAAGTGGCTTCGTGCACCCATGAAGCGGAGCAGAATGACTCTGTGAGCCCAAG 374
40 Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
41 12 LeuValIleuGlYThrAlaIatThrPheAspTrnAspProGluGuaIa---SerProArg 30
42
43 QY 375 AAATCCCAGATGGCGGGGCTCAAACCTCAGCTGAAGTGTTCTGTTGCCCTCAACAGGCTCTA 434
44 Db AAtgAAAtArghsheereeersearnserProserAspValAlaAhGysLeuAshnglyAlaIeu 50
45 31 ArgAlaArghsheereeersearnserProserAspValAlaAhGysLeuAshnglyAlaIeu 50
46
47 QY 435 CAGCTCGGCTGCGGGGCTTTGGCATGCCCTGAAAACTCCACTGTGACACAGATGGATG 494
48 Db CAgtTCGtGctgcggggctttggcatgccctgaaaaactccactgtgacacagatggatg 494
49 51 AlalvalglYsglythrPhelaGysLeuGluAnserThrcyAspThrAspGlyMet 70
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51 QY 495 TATGACATCTGTAAATCCTTCTGTATCACGCGTGTAAATTGTGACATCAGGAAAACA 554
52 Db ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
53 71 HisAspLecYsglnLeuPhePheHsthrAlaAlaIatThrPheAsnThrGlnGlyLeThr 90
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55 QY 555 TTCTGTCAAGAGAGCTTAAATGATGCATCGCCAAGGGGCTCACCTCCAGATCTTCTGACC 614
56 Db TTcTGTCAAGAGAGCTTAAATGATGCATCGCCAAGGGGCTCACCTCCAGATCTTCTGACC 614
57 91 PheValylsglInserIleuArGysIleAlaasnGlyValItnserLyvalPheGlnThr 110
58
59 QY 615 ATTCGAGGCTTCACATTTCCAAAGAGATGATGCTGAGGCTCAGAGAAAGTCTAACG 674
60 Db AtTCGaGGCTTCaCaTTTCCAAAGAGATGATGCTGAGGCTCAGAGAAAGTCTAACG 674
61 111 IleArGrArGysGslYalPheGlnAgMetIleSerGluValGlnGluGlyTySer 130
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63 QY 675 AAGCTGAATGTGTCAGCATGCGCAAGCGGAACCTCGAAGGCATCATCAGAGTGTCTCAG 734
64 Db AAGCTGAATGTGTCAGCATGCGCAAGCGGAACCTCGAAGGCATCATCAGAGTGTCTCAG 734
65 131 ArgLeuAspLecYsglyValAlaahgserranProGluAlaIleGlyGluValIaln 150
66
67 QY 735 CTGCCCCATCATCTTTCACACAGATATCTATAACAATTGTCGGAAGCTGTGGAATGT 794
68 Db CTGCCCCATCATCTTTCACACAGATATCTATAACAATTGTCGGAAGCTGTGGAATGT 794
69 151 ValPrroAlaHisPheTroAsnArgrYtyrTerThrIleuGlnSerIleuAlaGlys 170
70
71 QY 795 GAAGTAAGACACATCTGCGACAAATCAGAGACACCTCGATGAGAAATTTGGCCCTTAATG 854
72 Db GAAGTAAGACACATCTGCGACAAATCAGAGACACCTCGATGAGAAATTTGGCCCTTAATG 854
73 171 AspGluGlnIutrrValAlaValAlaGalaGlaGlyLeuValAlaahGluGlyProAspMet 190

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QY      955 GCGAGCCTCTTCACATCCGTGCGAGACAGCCACTGTGGCCCA 896
      191 GIunthreuehginleueneuGINenlyshIScSproGln 204

RESULT 8
US-08-460-529B-9
/ Sequence 9, Application US/08460529B
/ Patent No. 5994103
GENERAL INFORMATION:
APPLICANT: OLSEN, ET AL.
TITLE OF INVENTION: Human Stanniocalcin-alpha
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,529B
FILING DATE: June 2, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13206
FILING DATE: 10 NOV 1994
ATTORNEY/AGENT INFORMATION:
NAME: MULJINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-334 (PFI43)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ. ID NO.: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-460-529B-9

Alignment Scores:
Pred. No.: 2,59e-55 Length: 170
Score: 628.00 Matches: 113
Percent Similarity: 84.12% Conservative: 30
Best Local Similarity: 66.47% Mismatches: 27
Query Match: 9.19% Indels: 0
DB: 2 Gaps: 0

US-09-703-350B-75 (1-3900) x US-08-460-529B-9 (1-170)
QY      366 AGCCCCGAGAAATCCCGAGTGGCGGGCTCAAAATCAGCTGAGTGGTTCGCTTCAAC 4255
      1 SerProArgThrAlaIarPhseSerAlaSerSerProSerArgValAlaArgCysLeuAsn 20
QY      426 AGGCTCTTCAAGTGGCGTGGCGGGCTTTTGATGCGCTGAGAAATCCACTGTCGACCA 485
      21 G1yAlaIeudInAlaJcysSerAlaPheAlaCysLeuAparnserrThrCysAsnThr 40
Db      486 GATGGAGTATGATGACATCTGTAAATCCTTCTTGTAACAGCGCTGTAAATTGACACTGAG 545
      41 AspGlyMetHisGluIleCysArgSerPheLeuHisGlyAlaIalalysPheArgThrGln 60
QY      546 GGAAGACATCTGTCAAAAGAGCTTAAATATGCATCGCAACGGGCTCACTCCAGGTC 6055
      191 GIunthreuehginleueneuGINenlyshIScSproGln 204

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Db 61 GlyLeuThrPheValIysGluSerLeuLysCysIleAlaasnGlyIleThrSerIysVal 80  
QY 606 TTCTCGCCATTCGGAGGTCGTCCTCCACTTTCCTCAAGAGTATGCTGAGTGCAGAGAGG 665  
Db 81 PheLeuThrIleArgArgCysSerSerPheGlnIysMetIleSerGlnValGlnGln 100  
QY 666 TGTACAGAGAGTGTATGTGTGACAGATCGCCAGACCGCTTGAAGCCATCACTGAG 725  
Db 101 CysTyrSerIysLeuaspLeuLysSerValAlaGlnSerAsnProGlnIleIleGlyGln 120  
QY 726 GTGCTCCAGCTGCCCACTCACTTTCCTCAAGAGTATGCTGAGTGCAGAGAGG 785  
Db 121 ValAlaGlnValProSerGlnPheProAsnArgTyrTyrSerThrIleuGlnSerLeu 140  
QY 786 CTGGAATGTATGAAGACAGATGTCAGACATCAATCAGAGAGAGGCTGATGAGAAATTGGG 845  
Db 141 LeuThrCysAspGlnAspThrValGlnValArgAlaGlyLeuValSerArgLeuGln 160  
QY 846 CCTAACATGCGCCAGCTCTTCACATCCTG 875  
Db 161 ProGlnMetGlyValLeuPheGlnLeu 170  
RESULT 9  
US-09-361-736B-9  
; Sequence 9, Application US/09361736B  
; Patent No. 661877  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Human Stanniocalcin-Alpha  
; FILE REFERENCE: PFI43PDI1  
; CURRENT APPLICATION NUMBER: US/09/361,736B  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: 08/460,529  
; PRIOR FILING DATE: 1995-06-02  
; PRIOR APPLICATION NUMBER: PCT/ US94/13206  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 9  
; LENGTH: 170  
; TYPE: PRT  
; ORGANISM: Anguilla australis  
US-09-361-736B-9  
Alignment Scores:  
Pred. No.: 2,59e-55 Length: 170  
Score: 628.00 Matches: 113  
Percent Similarity: 84.12% Conservative: 30  
Best Local Similarity: 66.47% Mismatches: 27  
Query Match: 9.19% Indels: 0  
DB: 4 Gaps: 0  
US-09-703-350B-75 (1-3900) x US-09-361-736B-9 (1-170)  
QY 366 AGCCCCAGAGAAATCCCGAGGCGGCTCAAAACTGAGAGTGTGCTGCTCAAC 425  
Db 1 SerProArgThrAlaArgPheSerAlaSerProSerAspValAlaArgCysLeuAsn 20  
QY 426 AGTGCTTACAGGTCGGCTGGCGGGCTTTTGATGCTGCTGAAAACTCCACTGTGACACA 485  
Db 21 GlyAlaLeuGlnValAlaGlyCysSerAlaPheAlaCysLeuAspAsnSerThrCysAsnThr 40  
QY 486 GATGGATGATATGATCTGTAATCTCTTGTAGAGGCTGTAATTAATGACACTGAG 545  
Db 41 AspGlyMetHisIleIleCysArgSerPheLeuHisGlyAlaAlaLysPheAspThrGln 60  
QY 546 GGAAGAAGCATTCCTCAAGAGAGCTTAAATGATGATGCCAAGCGGGCTCACTCAAGGTC 605  
Db 61 GlyLeuThrPheValIysGluSerLeuLysCysIleAlaAsnGlyIleThrSerIysVal 80  
QY 606 TTCTCGCCATTCGGAGGTCGTCCTCCACTTTCCTCAAGAGTATGCTGAGTGCAGAGAGG 665  
Db 81 PheLeuThrIleArgArgCysSerSerPheGlnIysMetIleSerGlnValGlnGln 100

QY 666 TGTACAGAGAGTGTATGTGTGACAGATGCGCCAGAGGAGACCTGGAAGCCATCACTGAG 725  
Db 101 CysTyrSerIysLeuaspLeuLysSerValAlaGlnSerAsnProGlnIleIleGlyGln 120  
QY 726 GTGCTCCAGCTGCCCACTCACTTTCCTCAAGAGTATGCTGAGTGCAGAGAGG 785  
Db 121 ValAlaGlnValProSerGlnPheProAsnArgTyrTyrSerThrIleuGlnSerLeu 140  
QY 786 CTGGAATGTATGAAGACAGATGTCAGACATCAATCAGAGAGAGGCTGATGAGAAATTGGG 845  
Db 141 LeuThrCysAspGlnAspThrValGlnValArgAlaGlyLeuValSerArgLeuGln 160  
QY 846 CCTAACATGCGCCAGCTCTTCACATCCTG 875  
Db 161 ProGlnMetGlyValLeuPheGlnLeu 170  
RESULT 10  
US-08-831-132-2  
; Sequence 2, Application US/08831132  
; Patent No. 6008322  
; GENERAL INFORMATION:  
; APPLICANT: Kuestner, Rolf E.  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: Lok, Si  
; APPLICANT: Buddle, Michele  
; APPLICANT: Downey, William  
; TITLE OF INVENTION: STANNIOCALCIN-2  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/831,132  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sawislak, Deborah A.  
; REGISTRATION NUMBER: 37,438  
; REFERENCE/DOCKET NUMBER: 96-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6672  
; TELEFAX: 206-442-6678  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 302 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-831-132-2  
Alignment Scores:  
Pred. No.: 6.21e-28 Length: 302  
Score: 362.00 Matches: 88  
Percent Similarity: 50.00% Conservative: 47  
Best Local Similarity: 32.59% Mismatches: 110  
Query Match: 5.30% Indels: 25  
DB: 3 Gaps: 4  
US-09-703-350B-75 (1-3900) x US-08-831-132-2 (1-302)  
QY 276 TCTCAGAGAAATGCTCCAAACTCAGAGTGTGCTGCTGATC----- 323  
Db 3 AlaGlnArgLeuGlyGlnPheMetThrLeuAlaLeuValLeuAlaThrPheAspProAla 22

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QY 324 ---AGTCTTTGCAACCCATGAGGGGAG---CAGATGACTCTGTGAGCCCAAGAA 377
DB 23 ArgGlyThrAspAlaThrAsnProGluGlyProGlnAspArgSerSerGlnGlnLys 42
QY 378 TCCGAGTGGCGGCTCAAACTCAGCTGAGTGTCTGTTGCTGCTCAACAGTCTTCAAG 437
DB 43 GlyArgLeuSerLeuGlnInsnThrAlaGluIleGlnHisCysLeuValAsnAlaGlyAsp 62
QY 438 GTTGGCTGGGGGCTTTTGATGCTGTGAAAACCTCACTGTGACACAGATGGATGTAT 497
DB 63 ValGlyCysGlyValPheGluCysPheGluAsnAsnSerCysGluIleArgGlyLeuHis 82
QY 498 GACATCTGTAATCTCTTGTGACAGCTGCTAAATTGACATCCAGGAAAACATTC 557
DB 83 GlyIleCysMetThrPheLeuHisAsnAlaGlyLysPheAspAlaGlnGlyLysSerPhe 102
QY 558 GTCAAGAAGAGCTTAAATGATGATGCCCAAGGGGTCACTCCAGGTCTCTCCGCCATT 617
DB 103 IleLysAspAlaLeuLysCysLysAlaHisAlaIleuArgHisArgPheGlyCysIleSer 122
QY 618 CGGAGGTGGTCCGACTTTCAGAAAGATGATGCTGAGGTGACAGAGAGTGTACAGCAAG 677
DB 123 ArgLysCysProAlaIleArgGluMetValSerGlnLeuGlnArgGluCysArgLysLys 142
QY 678 CTGAATGTGTGACATGCCCAAGCGAAACCTGAAAGCCATGACTGAGGTCTGCAGCTG 737
DB 143 HisAspLeuCysAlaIleAlaIleGlnGluAsnThrArgValIleValGluMetIleHisPhe 162
QY 738 CCCAATCACTTCTCCCAACAGATACTATACAGACTTTGCTCCGAAAGCTGTGAAATGTAT 797
DB 163 LysAspLeuLeuLeuIleGluProGlyValAspLeuValAsnLeuLeuLeuThrCysGly 182
QY 798 GAAGACACAGTCAGCAATCAGAGACAGCTGATGAGAAATTTGGGCTTACATGAGCC 857
DB 183 GluGluValLysGluAlaIleThrHisSerValGlnValGlnCysGluGlnLysnThrPheGly 202
QY 858 AGCTCTTTCACATCTCTGCAAG--ACAGACCACTGTGCCCAACACACCCAGACTGAC 914
DB 203 SerLeuCysSerIleLeuSerPheCysThrIleSerAlaIleGlnLysProThrAlaPro 222
QY 915 TTCAAAGAGAGGACCAATGAGCCGAGAGCTG-----AAAGTCTCTTCAAGAACCTCCAGAGTACAG 950
DB 223 ProGluArgGlnProGluInValAspArgThrLysLeuSerArgAlaHisIleGlyAla 242
QY 951 -----AAAGTCTCTTCAAGAACCTCCAGAGTACAG 983
DB 243 GlyHisIleLeuProGluProSerSerArgGluThrGlyArgGlyAlaLysGlyLysArg 262
QY 984 GACTCTCCCTCCCAATCAAGCAATCAAGCAAT 1011
DB 263 GlySerLysSerHis-ProAsnAlaHis 271

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RESULT 11  
 US-09-416-150-2  
 Sequence 2, Application US/09416150  
 Patent No. 6171822  
 GENERAL INFORMATION:  
 APPLICANT: Kuestner, Rolf E.  
 Conklin, Darrell C.  
 Lok, Si  
 Buddle, Michele  
 Downey, William  
 TITLE OF INVENTION: STANNIOCALCIN-2  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ZymoGenetics, Inc.  
 STREET: 1201 Eastlake Avenue East  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98102  
 COMPUTER READABLE FORM:

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MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/416,150
  FILING DATE: 11-Oct-1999
  CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/831,132
    FILING DATE: <Unknown>
  ATTORNEY/AGENT INFORMATION:
    NAME: Sawislak, Deborah A.
    REGISTRATION NUMBER: 37,438
    REFERENCE/DOCKET NUMBER: 96-01
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 206-442-6672
    TELEFAX: 206-442-6678
  INFORMATION FOR SEQ ID NO: 2:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 302 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-416-150-2
Alignment Scores:
Pred. No.: 6,21e-28 Length: 302
Score: 362.00 Matches: 88
Percent Similarity: 50.00% Conservative: 47
Best Local Similarity: 32.59% Mismatches: 110
Query Match: 5.30% Indels: 25
Gaps: 4
US-09-703-350b-75 (1-3900) x US-09-416-150-2 (1-302)
QY 276 TCTGAGAGATNGCTCCAAACTCAGACAGTGTCTGTGCTGTGATC----- 323
DB 3 AlaGluArgLeuGluGlnPheMetThrLeuAlaLeuValLeuAlaThrPheAspProAla 22
QY 324 ---AGTCTTTGCAACCCATGAGGGGAG---CAGATGACTCTGTGAGCCCAAGAA 377
DB 23 ArgGlyThrAspAlaThrAsnProGluGlyProGlnAspArgSerSerGlnGlnLys 42
QY 378 TCCGAGTGGCGGCTCAAACTCAGCTGAGTGTCTGTTGCTGCTCAACAGTCTTCAAG 437
DB 43 GlyArgLeuSerLeuGlnInsnThrAlaGluIleGlnHisCysLeuValAsnAlaGlyAsp 62
QY 438 GTTGGCTGGGGGCTTTTGATGCTGTGAAAACCTCACTGTGACACAGATGGATGTAT 497
DB 63 ValGlyCysGlyValPheGluCysPheGluAsnAsnSerCysGluIleArgGlyLeuHis 82
QY 498 GACATCTGTAATCTCTTGTGACAGCTGCTAAATTGACATCCAGGAAAACATTC 557
DB 83 GlyIleCysMetThrPheLeuHisAsnAlaGlyLysPheAspAlaGlnGlyLysSerPhe 102
QY 558 GTCAAGAAGAGCTTAAATGATGATGCCCAAGGGGTCACTCCAGGTCTCTCCGCCATT 617
DB 103 IleLysAspAlaLeuLysCysLysAlaHisAlaIleuArgHisArgPheGlyCysIleSer 122
QY 618 CGGAGGTGGTCCGACTTTCAGAAAGATGATGCTGAGGTGACAGAGTGTACAGCAAG 677
DB 123 ArgLysCysProAlaIleArgGluMetValSerGlnLeuGlnArgGluCysArgLysLys 142
QY 678 CTGAATGTGTGACATGCCCAAGCGAAACCTGAAAGCCATGACTGAGGTCTGCAGCTG 737
DB 143 HisAspLeuCysAlaIleAlaIleGlnGluAsnThrArgValIleValGluMetIleHisPhe 162
QY 738 CCCAATCACTTCTCCCAACAGATACTATACAGACTTTGCTCCGAAAGCTGTGAAATGTAT 797
DB 163 LysAspLeuLeuLeuIleGluProGlyValAspLeuValAsnLeuLeuLeuThrCysGly 182

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QY 798 GAAGACAGCTCAGACATCAGACAGCTGATGGAGAAATGGAGCTTAACATGGCC 857
Db 183 GUGUVallysluValaIleThrhIsseValGlnValGlnCysgluInsnTrpGly 202
QY 858 AGCTCTTCCACATCCTGCGAG--ACAGACCATGTGCCCAACACACCCACGAGCTGAC 914
Db 203 SerLeuCyseIleLeuSerPheCysThrSerAlaIleGlnLysProProThraLapro 222
QY 915 TTCAAGAGGAGGACGACCATGAGCCGCAAGAGCTG----- 950
Db 223 ProGluArgGlnProGlnValAlaAspArgThrLysLeuSerArgAlaHisIleGlyGluAla 242
QY 951 -----AAAGTCCTCTCAGAAACCTCGAGGTGAGAG 983
Db 243 GLYHISHisleuProGluProSerSerArgGluThrGlyArgGlyAlaLysGlyGluArg 262
QY 984 GACTTCCTCCCTCCACATCAACGACAT 1011
Db 263 GlySerLysSerHis-ProAsnAlaHis 271

RESULT 12
US-09-193-881-23
; Sequence 23, Application US/09193881A
; Patent No. 6538119
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Colpitts
; APPLICANT: Paula N. Friedman
; APPLICANT: Edward N. Granados
; APPLICANT: Michael R. Klans
; APPLICANT: John C. Russell
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
; TITLE OF INVENTION: Breast
; FILE REFERENCE: 6248-US-P1
; CURRENT APPLICATION NUMBER: US/09/193,881A
; CURRENT FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-881-23

Alignment Scores:
Pred. No.: 6,21e-28 Length: 302
Score: 362.00 Matches: 88
Percent Similarity: 50.00% Conservative: 47
Best Local Similarity: 32.59% Mismatches: 110
Query Match: 5.30% Indels: 25
Gaps: 4

US-09-703-350B-75 (1-3900) x US-09-193-881-23 (1-302)
QY 276 TCTCAGAGATGCTCCAGAAACTCAGACAGTCTTGCTGCTGTATC----- 323
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QY 324 ---AGTGCTTGTCAACCCATGAGCGGAG---CAGATAGCTGTGTGAGCCCGAGAAA 377
Db 23 ArgGlyThrAspLathrasnProProGluGlyProGluAlaAspArgSerArgGlnLys 42
QY 378 TCCCGAGTGCGGCTCAAAATCTAGAGTGCTGCTGCTCAACAGTCTCTACAG 437
Db 43 GLYArgLeuSerLeuIleAsnThrAlaGluIleGlnHisCysLeuValAsnAlaGlyAsp 62
QY 438 GTGCGCTGCGGCTTTTGATGCTCTGAGAAATCTCACCTGTGACAGATGGATGAT 497
Db 63 ValGlyCysGlyAlaPheGluCysPheGluAsnAsnSerCysGluIleArgGlyLeuHis 82
QY 498 GACATCTGTAATCTTCTTTGACAGCGCTGCTAAATTTGACACTCAGGGAAGCATTC 557
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Db 83 GYLIECysMetThrPheLeuHisAsnAlaGlyLysPheAspAlaGlnGlyLysSerPhe 102
QY 558 GTCAAAAGAGCTTAAATGATCGCCAAACGGGCTCACTCCAAAGTCTTCTCGGCATT 617
Db 103 IleLysAspAlaLeuLysCysLysAlaHisAlaLeuArgHisArgPheGlyCysIleSer 122
QY 618 CGAGAGTCTCCACTTCCAAAGATGATGTGAGGTGCGAGAAAGTGTACAGCAG 677
Db 123 ArgLysCysProAlaIleArgGluMetValSerIleGlnArgGluCysIleLys 142
QY 678 CTGATGTGTGTCAGATCGCCAGCGGAGCCCTGAAGCATCACTGAGGTGTCAGCTG 737
Db 143 HisAspLeuCyseAlaAlaIleGlnGluAsnThrArgValIleValGluMetIleHisPhe 162
QY 738 CCCATCTCTTCTCCACAGATACTATPACAGACTTGTCCGAGCTGCTGGAATGTGAT 797
Db 163 LysAspLeuLeuLeuHisGlnProTrValAspLeuValLeuLeuThrCysGly 182
QY 798 GAAGACAGCTCAGACATCAGACAGCTGATGGAGAAATGGAGCTTAACATGGCC 857
Db 183 GUGUVallysluValaIleThrhIsseValGlnValGlnCysgluInsnTrpGly 202
QY 858 AGCTCTTCCACATCCTGCGAG--ACAGACCATGTGCCCAACACACCCACGAGCTGAC 914
Db 203 SerLeuCyseIleLeuSerPheCysThrSerAlaIleGlnLysProProThraLapro 222
QY 915 TTCAAGAGGAGGACGACCATGAGCCGCAAGAGCTG----- 950
Db 223 ProGluArgGlnProGlnValAlaAspArgThrLysLeuSerArgAlaHisIleGlyGluAla 242
QY 951 -----AAAGTCCTCTCAGAAACCTCGAGGTGAGAG 983
Db 243 GLYHISHisleuProGluProSerSerArgGluThrGlyArgGlyAlaLysGlyGluArg 262
QY 984 GACTTCCTCCCTCCACATCAACGACAT 1011
Db 263 GlySerLysSerHis-ProAsnAlaHis 271

RESULT 13
US-09-361-736B-12
; Sequence 12, Application US/09361736B
; Patent No. 6613877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stemlocalcin-Alpha
; FILE REFERENCE: PF143P1D1
; CURRENT APPLICATION NUMBER: US/09/361,736B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 302
; TYPE: PRT
; ORGANISM: human
US-09-361-736B-12

Alignment Scores:
Pred. No.: 6,21e-28 Length: 302
Score: 362.00 Matches: 88
Percent Similarity: 50.00% Conservative: 47
Best Local Similarity: 32.59% Mismatches: 110
Query Match: 5.30% Indels: 25
Gaps: 4

US-09-703-350B-75 (1-3900) x US-09-361-736B-12 (1-302)
QY 276 TCTCAGAGATGCTCCAGAAACTCAGACAGTCTTGCTGCTGTATC----- 323
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Db      3 AlaGluArgLeuGluGlnPheMetThrLeuAlaLeuValLeuAlaThrPheAspProAla 22
QY      324 ---AGTGGCTTTCGAACCCATGAGCGGAG---CAGATGACTCTGTGAGCCCGAGAAA 377
Db      23 ArgGlyThrAspAlaThrAsnProProGluGlyProGlnAspArgSerSerGlnGlnLys 42
QY      378 TCCCGAGTGGCGGCTCAAAACCTCAGTGAAGTGTGCTGTTGCTGCTCAACAGTCTCTACAG 437
Db      43 GlyArgLeuSerLeuGlnAsnThrAlaGluIleGlnHisCysLeuValAsnAlaGlyAsp 62
QY      438 GTCCGCTGCGGGCTTTTGCATGCTCTGAAAACTCCACCTGTGACACAGATGGATGAT 497
Db      63 ValGlyCysGlyValAlaPheGluCysPheGluAsnAsnSerCysGluIleArgGlyLeuHis 82
QY      498 GACATTTGTAATTCCTTTGTGAACAGCGCTGTAATTGACATCAGAGGAAACATTC 557
Db      83 GlyIleCysMetThrPheLeuHisAsnAlaGlyLysPheAspAlaGlnIleLysSerPhe 102
QY      558 GTCCAAAGAGAGCTTAAATATGATCGCCAAACGAGGTGACCTCCAGGTCTTCTGCGCAT 617
Db      103 IleValAspAlaLeuLysCysLysAlaHisAlaLeuAlaGlnHisArgPheGlyCysLieser 122
QY      618 CGAGGTGCTGCCCTTTCCAAAGAGATGATGCTGAGGTGACAGAGAGAGTCTACAGAG 677
Db      123 ArgLysCysProAlaIleArgGluMetValIserGlnLeuGlnArgGluCysTyrLeuLys 142
QY      678 CTGAATGTGTGACGATCGCCAAACCGGAAACCTGAAAGCCATCATGAGGTCTGTCAGCTG 737
Db      143 HisAspLeuCysAlaIleAlaIleGlnGlnValAsnThrArgValIleValGluMetIleHisPhe 162
QY      738 CCCATCATCTTCTCCAAACAGATCTTAAACAGATTTGCTCGAAGCTGTGTGAAATGTGAT 797
Db      163 LysAspLeuLeuLeuHisGluProTyrValAspLeuValAsnLeuLeuLeuThrCysGly 182
QY      798 GAAGACACAGTCACGACCAATTCAGACAGCGCTGATGAGAAATTGGCGCTTAACATGGCC 857
Db      183 GlnGlnValLysGlnAlaIleThrHisSerValGlnValGlnCysGlnAsnThrArgLys 202
QY      858 AGCCTCTTCCACATCTCTGAG--ACAGACCACTGTGCCAAACACACCCACAGAGCTGAC 914
Db      203 SerLeuCysSerIleLeuSerPheCysThrSerAlaIleGlnLysProProThrAlaPro 222
QY      915 TTCACAGAGAGAGCCCAATGAGCGGCAAGAGCTG----- 950
Db      223 ProGluArgGlnProGlnValAspArgThrLysLeuSerArgAlaHisIleGlyAla 242
QY      951 -----AAAGTCTCTCCAGGAACCTCCAGAGTACAGAG 983
Db      243 GlyHisIleSerProGluProSerSerArgGluThrGlyArgGlyAlaLysGlyGlnArg 262
QY      984 GACTCTCCCTCCCAACATCAAAAGCCACAT 1011
Db      263 GlySerLysSerHis-ProAsnAlaHis 271

RESULT 14
US-09-361-736B-2
; Sequence 2, Application US/09361736B
; Patent No. 6618877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Staminalcain-Alpha
; FILE REFERENCE: PFI43PDI1
; CURRENT APPLICATION NUMBER: US/09/361, 736B
; PRIORITY FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460, 529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 251
; TYPE: PRT

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; ORGANISM: human
US-09-361-736B-2

Alignment Scores:
Pred. No.: 2,05e-27
Score: 356.50
Percent Similarity: 53.17%
Best Local Similarity: 34.52%
Query Match: 5.22%
DB: 4 Gaps: 6

US-09-703-350B-75 (1-3900) x US-09-361-736B-2 (1-251)

QY      276 TCTCAGAGAAATGCTCCAAAACCTCAGACAGTGTCTGTGCTGTGATC----- 323
Db      3 AlaGluArgLeuGluGlnPheMetThrLeuAlaLeuValLeuAlaThrPheAspProAla 22
QY      324 ---AGTGGCTTTCGAACCCATGAGCGGAG---CAGATGACTCTGTGAGCCCGAGAAA 377
Db      23 ArgGlyThrAspAlaThrAsnProProGluGlyProGlnAspArgSerSerGlnGlnLys 42
QY      378 TCCCGAGTGGCGGCTCAAAACCTCAGTGAAGTGTGCTGTTGCTGCTCAACAGTCTCTACAG 437
Db      43 GlyArgLeuSerLeuGlnAsnThrAlaGluIleGlnHisCysLeuValAsnAlaGlyAsp 62
QY      438 GTCCGCTGCGGGCTTTTGCATGCTCTGAAAACTCCACCTGTGACACAGATGGATGAT 497
Db      63 ValGlyCysGlyValAlaPheGluCysPheGluAsnAsnSerCysGluIleArgGlyLeuHis 82
QY      498 GACATTTGTAATTCCTTTGTGAACAGCGCTGTAATTGACATCAGAGGAAACATTC 557
Db      83 GlyIleCysMetThrPheLeuHisAsnAlaGlyLysPheAspAlaGlnIleLysSerPhe 102
QY      558 GTCCAAAGAGAGCTTAAATATGATCGCCAAACGAGGTGACCTCCAGGTCTTCTGCGCAT 617
Db      103 IleValAspAlaLeuLysCysLysAlaHisAlaLeuAlaGlnHisArgPheGlyCysLieser 122
QY      618 CGAGGTGCTGCCCTTTCCAAAGAGATGATGCTGAGGTGACAGAGAGAGTCTACAGAG 677
Db      123 ArgLysCysProAlaIleArgGluMetValIserGlnLeuGlnArgGluCysTyrLeuLys 142
QY      678 CTGAATGTGTGACGATCGCCAAACCGGAAACCTGAAAGCCATCATGAGGTCTGTCAGCTG 737
Db      143 HisAspLeuCysAlaIleAlaIleGlnGlnValAsnThrArgValIleValGluMetIleHisPhe 162
QY      738 CCCATCATCTTCTCCAAACAGATCTTAAACAGATTTGCTCGAAGCTGTGTGAAATGTGAT 797
Db      163 LysAspLeuLeuLeuHisGluProTyrValAspLeuValAsnLeuLeuLeuThrCysGly 182
QY      798 GAAGACACAGTCACGACCAATTCAGACAGCGCTGATGAGAAATTGGCGCTTAACATGGCC 857
Db      183 GlnGlnValLysGlnAlaIleThrHisSerValGlnValGlnCysGlnAsnThrArgLys 202
QY      858 AGCCTCTTCCACATCTCTGAGACAGACCACTGTGCC-----CAAACACCCACGA 908
Db      203 SerLeuCysSerIleLeu-----SerPheCysThrSerAlaIleGlnLysProProThr 220
QY      909 GCTGACTTCAACAGAGAGAGCAACCAATGAGCGGAG-----AAAGTCAAGTCTCTCTC 962
Db      221 AlaProProGluArg-----GlnProGlnValAspArgThrLysLeuSerArg 236
QY      963 AGGAACCTCCAGGTGAGAGAGACTCTCTCC 996
Db      237 AlaHisIleGlyGly-ArgArgThrSerProPro 247

RESULT 15
US-08-831-132-14
; Sequence 14, Application US/08831132
; Patent No. 6008322
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lok, Si

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/ APPLICANT: Buddle, Michele
/ APPLICANT: Downey, William
/ TITLE OF INVENTION: STANNICALCIN-2
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Zymogenetics, Inc.
/ STREET: 1201 Eastlake Avenue East
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98102
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/831,132
/ FILING DATE:
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sawislak, Deborah A.
/ REGISTRATION NUMBER: 37,458
/ REFERENCE/DOCKET NUMBER: 96-01
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-442-6672
/ TELEFAX: 206-442-6678
/ INFORMATION FOR SEQ. ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 296 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-831-132-14

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Score: 356.00 Matches: 84
Percent Similarity: 49.42% Conservative: 44
Best Local Similarity: 32.43% Mismatches: 106
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DB: 3 Gaps: 4

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US-09-703-350b-75 (1-3900) x US-08-831-132-14 (1-296)

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Db 88 PheLeuHisAsnAlaGlyCysPheAspAlaGlnGlyLysSerPheIleLysAspAlaLeu 107
QY 573 AAATGATCGCCCAACGGGGTCACTCCAAAGTCTTCTCGCCATTGCGAGAGTCTCCACT 632
Db 108 ArgCysLeuAlaHisAlaLeuArgHisLysPheGlyCysIleSerArgLysCysProAla 127
QY 633 TTCCAAAGGATGATTGGTGAAGTGCAGAAAGAGTCTACAGCAAGCTGAATGTGTGACG 692
Db 128 IleArgGlnMetValPheGlnLeuGlnArgGlnCysArgLysLeuValHisAspLeuCysSer 147

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QY 693 ATCCCAAGCGGAACCTGAAACCATCACTGAGTGTCTCCAGCTGCCCAATCACTTCTCC 752
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Search completed: November 16, 2004, 08:53:04  
Job time : 95 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: November 16, 2004, 08:46:07 ; Search time 448 Seconds  
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Ygapop 10.0 , Ygapext 0.5  
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Delop 6.0 , Delext 7.0

Searched: 1566699 segs, 35381937 residues

Total number of hits satisfying chosen parameters: 3137398

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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Published Applications AA: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

Result Query \* SUMMARIES

No.	Score	Match	Length	DB	ID	Description
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2	1268	18.6	247	9	US-09-840-989A-2	Sequence 2, Appl
3	1268	18.6	247	9	US-09-361-736-10	Sequence 10, Appl
4	1268	18.6	247	13	US-10-116-051-2	Sequence 2, Appl
5	1268	18.6	247	14	US-10-177-293-441	Sequence 441, Appl
6	1268	18.6	247	14	US-10-418-226-10	Sequence 10, Appl
7	1268	18.6	247	14	US-10-465-572-18	Sequence 18, Appl
8	1268	18.6	247	15	US-10-372-683-41	Sequence 41, Appl
9	1268	18.6	247	17	US-10-614-990-2	Sequence 2, Appl
10	662.5	9.7	256	9	US-09-840-989A-3	Sequence 3, Appl
11	662.5	9.7	256	17	US-10-614-990-3	Sequence 3, Appl
12	660.5	9.7	204	13	US-10-116-051-10	Sequence 10, Appl
13	628	9.2	170	9	US-09-361-736-9	Sequence 9, Appl
14	628	9.2	170	14	US-10-418-226-9	Sequence 9, Appl
15	362	5.3	302	9	US-09-193-881-23	Sequence 23, Appl
16	362	5.3	302	14	US-10-177-293-443	Sequence 443, Appl
17	362	5.3	302	14	US-10-338-395-23	Sequence 23, Appl
18	362	5.3	302	14	US-10-418-226-12	Sequence 12, Appl
19	362	5.3	302	14	US-10-364-889-4	Sequence 4, Appl
20	362	5.3	302	14	US-10-295-027-100	Sequence 100, Appl
21	362	5.3	302	15	US-10-173-999-80	Sequence 80, Appl
22	362	5.3	302	15	US-10-058-270A-22	Sequence 22, Appl
23	358	5.2	70	9	US-09-864-761-37770	Sequence 37770, A
24	356.5	5.2	251	14	US-10-418-226-2	Sequence 2, Appl
25	338.5	5.0	251	14	US-09-361-736-2	Sequence 2, Appl
26	303	4.4	118	13	US-10-116-051-9	Sequence 9, Appl
27	200	2.7	34	9	US-10-029-386-33022	Sequence 33022, A
28	187	2.7	34	9	US-09-864-761-37771	Sequence 37771, A
29	184	2.7	966	9	US-09-801-368-372	Sequence 372, App
30	184	2.7	966	16	US-10-451-467A-52	Sequence 52, Appl
31	182.5	2.6	1760	14	US-10-123-155-5	Sequence 5, Appl
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33	182.5	2.6	1760	14	US-10-140-472-5	Sequence 5, Appl
34	182.5	2.6	1760	14	US-10-141-761-5	Sequence 5, Appl
35	182.5	2.6	1760	14	US-10-142-885-5	Sequence 5, Appl
36	182.5	2.6	1760	14	US-10-158-790-5	Sequence 5, Appl
37	182.5	2.6	1760	14	US-10-137-871-5	Sequence 5, Appl
38	182.5	2.6	1760	14	US-10-140-923-5	Sequence 5, Appl
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42	182.5	2.6	1760	14	US-10-140-864-5	Sequence 5, Appl
43	182.5	2.6	1760	15	US-10-142-426-5	Sequence 5, Appl
44	181	2.6	71	16	US-10-437-963-105846	Sequence 105846,
45	180.5	2.6	4185	14	US-10-123-155-67	Sequence 67, Appl

## ALIGNMENTS

US-09-925-300-1426  
; Sequence 1426, Application US/099253300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen,  
; APPLICANT: Steve Ruden,  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA101  
; CURRENT APPLICATION NUMBER: US/09/925.300  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05988  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; NUMBER OF SEQ ID NOS: 1890  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1426  
; LENGTH: 276  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:

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: NAME/KEY SITE
: LOCATION: (43)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
:
: NAME/KEY SITE
: LOCATION: (273)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY SITE
: LOCATION: (275)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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: US-09-925-300-1426

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Best Local Similarity:	99.27%
Query Match:	20.54%
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Conservative:	0
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Indels:	0
Gaps:	0

US-09-703-350B-75 (1-3900) x US-09-925-300-1426 (1-276)

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## RESULT 2

US-09-840-989A-2  
; Sequence 2, Application US/09840989A

Patent No. US20020042372A1

GENERAL INFORMATION:

APPLICANT: Olsell et al.

FILE REFERENCE: PF108P2

CURRENT APPLICATION NUMBER: US/09/840,989A

CURRENT FILING DATE: 2001-04-25

PRIOR APPLICATION NUMBER: PCT/US00/29432

PRIOR FILING DATE: 2000-10-26  
 PRIOR ADDITION NUMBER: YES 00/161 740

PRIOR FILING DATE: 1999-10-27

NUMBER OF SEO ID NOS: 12

SOFTWARE: PatentIn version 3.1.1

SEQ ID NO 2

LENGTH: 247

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; TYPE: PRT
OCCURANCE Times

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ORGANISM: Homo sapiens  
MS-09-840-989A-2

05-00-040-0000

### Alignment Scores

Pred. No.:

Score: \_\_\_\_\_

Percent Similarity

Best Local Siml

Query Mail: DR.

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US-09-703-350B-75 (1-3900) x US-09-840-989A-2 (1-247)

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 QY 945 AAGCTGAAGTCTCTCTCGAAGCTCCGAGGTGAGAGAGACTCTCCCTCCCAATCAAA 1004  
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 QY 1005 CGACATCCCATGAGAGTGCA 1025  
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 RESULT 3  
 US-09-361-736-10  
 ; Sequence 10, Application US/09361736  
 ; Patent No. US20020102634A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OLSEN, ET AL.  
 ; TITLE OF INVENTION: Human Stanniocalcin-alpha  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: CECCHI, BYRNE, BAIN, GILFILLAN,  
 ; ADDRESS: 6 BECKER FARM ROAD  
 ; STREET: 6 BECKER FARM ROAD  
 ; CITY: ROSELAND  
 ; STATE: NEW JERSEY  
 ; COUNTRY: USA  
 ; ZIP: 07068  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 INCH DISKETTE  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: WORD PERFECT 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/361,736  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/460,529  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: MULLINS, J.G.  
 ; REGISTRATION NUMBER: 33,073  
 ; REFERENCE/DOCKET NUMBER: 325600-334 (PFI43)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 201-994-1700  
 ; TELEFAX: 201-994-1744  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 247 AMINO ACIDS  
 ; TYPE: AMINO ACID  
 ; STRANDEDNESS:  
 ; TOPOLOGY: LINEAR  
 ; MOLECULE TYPE: PROTEIN  
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 QY 885 CACTGTGCCCAACACACCCAGAGTGAATTCACACAGAGACGACCAATGAGCCGAG 944  
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 QY 945 AAGCTGAAGTCTCTCTCGAAGCTCCGAGGTGAGAGAGACTCTCCCTCCCAATCAAA 1004  
 DB 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240  
 QY 1005 CGACATCCCATGAGAGTGCA 1025  
 DB 241 ArgThrSerHisGluSerAla 247  
 RESULT 4  
 US-10-116-051-2  
 ; Sequence 2, Application US/10116051  
 ; Publication No. US20020146791A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OLSEN et al.  
 ; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN  
 ; FILE REFERENCE: PFI08PIDICT  
 ; CURRENT APPLICATION NUMBER: US/10/116,051  
 ; CURRENT FILING DATE: 2002-04-05  
 ; PRIOR APPLICATION NUMBER: 09/312,610  
 ; PRIOR FILING DATE: 1999-05-17  
 ; PRIOR APPLICATION NUMBER: 08/431,117  
 ; PRIOR FILING DATE: 1995-04-28  
 ; PRIOR APPLICATION NUMBER: 08/208,005  
 ; PRIOR FILING DATE: 1994-03-08  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 247  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-116-051-2  
 Alignment Scores:

Pred. No.: 3,978-106 Length: 247  
 Score: 1268.00 Matches: 247  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 18,568 Indels: 0  
 DB: 13 Gaps: 0

US-09-703-350B-75 (1-3900) x US-10-116-051-2 (1-247)

QY 285 ATGCTCCAAACTCAGCAGGCTTGTGCTGCTGATGATGATGCTTGTGCAACCATGAG 344  
 DB 1 MetLeuGlnAsnSerIleValIleuLeuValIleSerIleSerIleThrIleGlu 20  
 QY 345 GCGGAGCAGATGACTCTGTGAGCCCGAGAAATCCGAGTGGCGCTCAAACTGAGCT 404  
 DB 21 AlaGlnGlnAsnSerValSerProArgIlySerArgValAlaAlaGlnAsnSerAla 40  
 QY 405 GAAGTGGTTCGCTGCTCAACAGTGTCTCAACAGTGTGCTGCGGGGCTTTTCATGCGCTG 464  
 DB 41 GluValValArgCysLeuAsnSerIleAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60  
 QY 465 GAAACTCCACCTGTGACACAGATGGATGTATGATCATCTGTAAATCTTCTTGTACAGC 524  
 DB 61 GluAsnSerThrCysAspThrAspGlyMetIlyrAspIleCysIlySerPheLeuIlySer 80  
 QY 525 GCTGCTAAATTTGACACTCAGGAGAAAGCATTCGTCAAGAGAGCTTAAATGCATCCGC 584  
 DB 81 AlaAlaIlyPheAspThrGlnGlyIlyValAlaPheValIlyGlnSerLeuIlyCysIleAla 100  
 QY 585 AACGGGGTCACTCCAGAGCTTCTCCGCAATTCGAGGCTGCTCCACTTCCAAAGATG 644  
 DB 101 AsnGlyValThrSerIlyValPheLeuAlaIleArgIlyCysSerThrPheGlnArgMet 120  
 QY 645 ATTGCTGAGGTGACAGAAAGTGTCTACAGCAAGCTGATGTGTGACATGCCCAAGCGG 704  
 DB 121 IleAlaGlnValGlnGlnIlyCysIlySerIlyLeuAsnValCysSerIleAlaIlyAsnArg 140  
 QY 705 AACCTGAGAGCCATCACTGAGGTGCTGCTGAGCCCAATCTTCTCCAAAGATATCAT 764  
 DB 141 AsnProGlnAlaIleThrGlnValValGlnLeuProAsnIlyPheSerAsnArgIlyTrp 160  
 QY 765 AACAGACTTGTCCGAAAGCTGTGAAATGTATGAAGACAGTCAAGCAATCCAGAGAC 824  
 DB 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGlnAspThrValSerThrIleArgAsp 180  
 QY 825 AGCTGATGAGAGAAATTTGGGCTTAACATGGCCAGGCTTCTTCATCTGTCAGACAGAC 884  
 DB 181 SerLeuMetGlnIlyIleGlyProAsnMetAlaSerLeuPheIleIleuGlnThrAsp 200  
 QY 885 CACTGTGCCCAACACACACCCAGAGCTTCAACAGAGAGACCAATGAGCCGAG 944  
 DB 201 HisCysAlaGlnThrHisProArgIleAspPheAsnArgArgThrAsnGlnProGln 220  
 QY 945 AAGCTGAAAGTCTCTCTCAAGAACTCCGAGGTGAGAGAGATCTCCCTCCACATCAA 1004  
 DB 221 LysLeuIlyValIleuLeuArgAsnLeuArgIlyGlnGlnAspSerProSerHisIleLys 240  
 QY 1005 CGCAGATCCCATGAGAGTGCA 1025  
 DB 241 ArgThrSerHisGluSerAla 247

RESULT 5  
 US-10-177-293-441  
 ; Sequence 441, Application US/10177293  
 ; Publication No. US20030124128A1

; GENERAL INFORMATION:  
 ; APPLICANT: Lillie, James  
 ; APPLICANT: Glate, Karen  
 ; APPLICANT: Zhao, Xumei  
 ; APPLICANT: Gannavarapu, Manjula  
 ; APPLICANT: Kamatkar, Shubhangi  
 ; APPLICANT: Mertens, Maureen  
 ; APPLICANT: Myer, Vic

; APPLICANT: Wang, Youzhen  
 ; APPLICANT: Xu, Yongyao  
 ; APPLICANT: Hoersch, Sebastian  
 ; APPLICANT: Monahan, John  
 ; APPLICANT: Meyers, Rachel B.  
 ; APPLICANT: Basc Jr., Robert C.  
 ; APPLICANT: Hortobagyi, Gabriel N.  
 ; APPLICANT: Puzetal, Lajos  
 ; APPLICANT: Meric, Funda  
 ; APPLICANT: Sahin, Aysegul  
 ; APPLICANT: Mills, Gordon B.  
 ; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,  
 ; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER  
 ; FILE REFERENCE: MRI-038  
 ; CURRENT APPLICATION NUMBER: US/10/177,293  
 ; PRIOR FILING DATE: 2002-06-21  
 ; PRIOR APPLICATION NUMBER: US 60/299,887  
 ; PRIOR FILING DATE: 2001-06-21  
 ; PRIOR APPLICATION NUMBER: US 60/301,572  
 ; PRIOR FILING DATE: 2001-06-27  
 ; PRIOR APPLICATION NUMBER: US 60/306,501  
 ; PRIOR FILING DATE: 2001-07-18  
 ; PRIOR APPLICATION NUMBER: US 60/325,002  
 ; PRIOR FILING DATE: 2001-09-25  
 ; PRIOR APPLICATION NUMBER: US 60/362,585  
 ; PRIOR FILING DATE: 2002-03-05  
 ; PRIOR APPLICATION NUMBER: US 60/xxx,xxx  
 ; PRIOR FILING DATE: 2002-05-14  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 441  
 ; LENGTH: 247  
 ; TYPE: PRF  
 ; ORGANISM: Homo sapiens  
 ; US-10-177-293-441

Alignment Scores:  
 Pred. No.: 3,978-106 Length: 247  
 Score: 1268.00 Matches: 247  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 18,568 Indels: 0  
 DB: 14 Gaps: 0

US-09-703-350B-75 (1-3900) x US-10-177-293-441 (1-247)

QY 285 ATGCTCCAAACTCAGCAGGCTTGTGCTGCTGATGATGATGCTTGTGCAACCATGAG 344  
 DB 1 MetLeuGlnAsnSerIleValIleuLeuValIleSerIleSerIleThrIleGlu 20  
 QY 345 GCGGAGCAGATGACTCTGTGAGCCCGAGAAATCCGAGTGGCGCTCAAACTGAGCT 404  
 DB 21 AlaGlnGlnAsnSerValSerProArgIlySerArgValAlaAlaGlnAsnSerAla 40  
 QY 405 GAAGTGGTTCGCTGCTCAACAGTGTCTCAACAGTGTGCTGCGGGGCTTTTCATGCGCTG 464  
 DB 41 GluValValArgCysLeuAsnSerIleAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60  
 QY 465 GAAACTCCACCTGTGACACAGATGGATGTATGATCATCTGTAAATCTTCTTGTACAGC 524  
 DB 61 GluAsnSerThrCysAspThrAspGlyMetIlyrAspIleCysIlySerPheLeuIlySer 80  
 QY 525 GCTGCTAAATTTGACACTCAGGAGAAAGCATTCGTCAAGAGAGCTTAAATGCATCCGC 584  
 DB 81 AlaAlaIlyPheAspThrGlnGlyIlyValAlaPheValIlyGlnSerLeuIlyCysIleAla 100  
 QY 585 AACGGGGTCACTCCAGAGCTTCTCCGCAATTCGAGGCTGCTCCACTTCCAAAGATG 644  
 DB 101 AsnGlyValThrSerIlyValPheLeuAlaIleArgIlyCysSerThrPheGlnArgMet 120  
 QY 645 ATTGCTGAGGTGACAGAAAGTGTCTACAGCAAGCTGATGTGTGACATGCCCAAGCGG 704  
 DB 121 IleAlaGlnValGlnGlnIlyCysIlySerIlyLeuAsnValCysSerIleAlaIlyAsnArg 140

QY 705 AACCTGAAGCCATCTGAGGTCGCTGAGTCCCAATCACTTCTCCACAGATACTAT 764  
 Db 141 AAsnProGluAlaIleThrGluValValGlnLeuProMetHisPheSerAsnArgTyr 160  
 QY 765 AACAGACTGTCCGAAAGCTGTGTGAATGTATGAAGACACAGTGCAGCAATCAAGAGAC 824  
 Db 161 AsnArgLeuValAlaArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgasp 180  
 QY 825 AGCTGTATGAGAAATTTGGGCTTAACATGGCCAGCTCTTCCACATCCCTGACAGACAG 884  
 Db 181 SerLeuMetGluLysIleGlyProMetMetAlaSerLeuPheHisIleLeuGlnThrAsp 200  
 QY 885 CACTGTGCCCAACACACCCACGAGCTGACTTCAACAGAGAGACGACCAATGAGCCGACG 944  
 Db 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220  
 QY 945 AAGCTGAAGTCTCTCTCAAGAACTCCGAGGTGAGAGAGACTCTCCCTCCACATCAAA 1004  
 Db 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240  
 QY 1005 CGCACATCCCATGAGAGTGCA 1025  
 Db 241 ArgThrSerHisGluSerAla 247

RESULT 6  
 US-10-418-226-10  
 ; Sequence 10, Application US/10418226  
 ; Publication No. US20030181663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Human Genome Sciences, Inc.  
 ; TITLE OF INVENTION: Human Stemcellcin-Alpha  
 ; FILE REFERENCE: Ff143P1D2  
 ; CURRENT APPLICATION NUMBER: US/10/418, 226  
 ; PRIOR FILING DATE: 2003-04-18  
 ; PRIOR APPLICATION NUMBER: 09/361, 736  
 ; PRIOR FILING DATE: 1999-07-28  
 ; PRIOR APPLICATION NUMBER: 08/460, 529  
 ; PRIOR FILING DATE: 1995-06-02  
 ; PRIOR APPLICATION NUMBER: PCT/ US94/13206  
 ; PRIOR FILING DATE: 1994-11-30  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 10  
 ; LENGTH: 247  
 ; TYPE: PRT  
 ; ORGANISM: human  
 ; US-10-418-226-10

Alignment Scores:  
 Pred. No.: 3,97e-106 Length: 247  
 Score: 1268.00 Matches: 247  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 18.56% Indels: 0  
 DB: 14 Gaps: 0

US-09-703-350b-75 (1-3900) x US-10-418-226-10 (1-247)

QY 285 ATGCTCCAAACTCAGCAGTGTCTTGTGTGTGTGTATCAGTGTCTTTCGAACCATGAG 344  
 Db 1 MetLeuGlnAsnSerAlaValLeuLeuValIleValIleSerAlaSerAlaThrHisGlu 20  
 QY 345 GCGGACAGATGACTCTGTGAGAGCCCGAGAAATCCCGAGTGGCGGCTCAAAATCAGCT 404  
 Db 21 AlaGluGlnAsnAspSerValSerProAlaGlySerArgValAlaAlaGlnAsnSerAla 40  
 QY 405 GAAGTGGTTCGTCTCAACAGTGTCTTACAGTGTGGCTGGGGCTTTTTCATGCTTG 464  
 Db 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60  
 QY 465 GAAATCCCACTGTGACACAGATGGAGTATGACATCTGTAATCTTCTTGTACAGC 524

Db 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysIysSerPheLeuTyrSer 80  
 QY 525 GCTGCTAAATTTGACACTCAGAGGAAAGACTTGTCATAAGAGAGCTTAAATGATCGCC 584  
 Db 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100  
 QY 585 AACGGGCTACCTTCGAAGTCTTCTCTGCGCATTCGAGGTGCTTCACCTTTCGAAGATG 644  
 Db 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120  
 QY 645 ATTGCTGAGGTGCGAGAAAGTGTCTACAGCAAGCTGAATGTGCGACATCGCAAGCGG 704  
 Db 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140  
 QY 705 AACCTGAAGCCATCACTGAGTGTGTCAGCTGCGCCATCACTTCTGCAACAGATACTAT 764  
 Db 141 AAsnProGluAlaIleThrGluValValGlnLeuProMetHisPheSerAsnArgTyr 160  
 QY 765 AACAGACTGTTCGCAAGCTGTGTGAATGTATGAAGACACAGTGCAGACCAATCAAGAGAC 824  
 Db 161 AsnArgLeuValAlaArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgasp 180  
 QY 825 AGCTGTATGAGAAATTTGGGCTTAACATGGCCAGCTCTTCCACATCTGACAGACAGAC 884  
 Db 181 SerLeuMetGluLysIleGlyProMetMetAlaSerLeuPheHisIleLeuGlnThrAsp 200  
 QY 885 CACTGTGCCCAACACACCCACGAGCTGACTTCAACAGAGAGACGACCAATGAGCCGACG 944  
 Db 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220  
 QY 945 AAGCTGAAGTCTCTCTCAAGAACTCCGAGGTGAGAGAGACTCTCCCTCCACATCAAA 1004  
 Db 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240  
 QY 1005 CGCACATCCCATGAGAGTGCA 1025  
 Db 241 ArgThrSerHisGluSerAla 247

RESULT 7  
 US-10-465-572-18  
 ; Sequence 18, Application US/10465572  
 ; Publication No. US20030207840A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Riggs, Gregory  
 ; APPLICANT: Lal, Anita  
 ; TITLE OF INVENTION: GENES INDUCED BY HYPOXIA  
 ; FILE REFERENCE: 000250.00012  
 ; CURRENT APPLICATION NUMBER: US/10/465, 572  
 ; PRIOR FILING DATE: 2003-06-20  
 ; PRIOR APPLICATION NUMBER: US/10/201, 642  
 ; PRIOR FILING DATE: 2002-07-24  
 ; PRIOR APPLICATION NUMBER: 60/307, 600  
 ; PRIOR FILING DATE: 2001-07-26  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 18  
 ; LENGTH: 247  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-465-572-18

Alignment Scores:  
 Pred. No.: 3,97e-106 Length: 247  
 Score: 1268.00 Matches: 247  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 18.56% Indels: 0  
 DB: 14 Gaps: 0

US-09-703-350b-75 (1-3900) x US-10-465-572-18 (1-247)

QY 285 ATGCTCCAAACTCAGCAGTGTCTTGTGTGTGTGTATCAGTGTCTTTCGAACCATGAG 344

Db 1 MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20  
 QY 345 GCGAGACAGAAATGACTCTGTGAGCCCGAGAAATCCCGAGTGGCGCTCAAAATCACT 404  
 Db 21 AlaGlnGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnSerAla 40  
 QY 405 GAAAGTGTGCTGCTTCAACAGTGTCTTACAGTGTGGTGGGGGCTTTTCATGCTGTG 464  
 Db 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60  
 QY 465 GAAATCCACCTGACACAGATGGATGTATGACATCTGTAATCCCTTTGTACAGC 524  
 Db 61 GluAsnSerThrCysAspThrAspGlyMetLysPheIleCysLysSerPheLeuYrSer 80  
 QY 525 GCTGCTAAATTTGACACTCAGGAGAAAGATTGCTCAAAAGAGACTTAAATGCATCGCC 584  
 Db 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100  
 QY 585 AACGGGCTACCTCCAGAGTCTTCCGCGCATTCGAGAGTGTCCACTTCCAAAGATG 644  
 Db 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120  
 QY 645 ATTGCTAGAGTGCAGAGAGAGTGTCTACAGCAAGCTGAATGTGTGACAGATCGCAAGCGG 704  
 Db 121 IleAlaGlnValGlnGlnGlnCysLysSerLysLeuAsnValCysSerIleAlaLysArg 140  
 QY 705 AACCCGTAAGCATCACTGAGTGTGCTGCGCCGCGCATCTTCCAAAGATATCAT 764  
 Db 141 AspProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgLysTyr 160  
 QY 765 AACAGACTGTGCTCGAAGCTGTGTAATGTGATGAAGACACAGTGCAGACATCAGAGAC 824  
 Db 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGlnAspThrValSerThrIleArgAsp 180  
 QY 825 AGCTGTATGAGAAATTTGGGCTTAACATGGCCAGCTTCTTCCAACTCTGACAGCAAC 884  
 Db 181 SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200  
 QY 885 CACTGTGCCCAACACACACAGAGTGTCTCAACAGAGAGACCAATAGCCGAG 944  
 Db 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlnProGln 220  
 QY 945 AAGCTGAAGTCTCTCTCGAGAACTCCGAGGTGAGAGAGACTCTTCCCTCCCATCAAA 1004  
 Db 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGlnAspSerProSerHisIleLys 240  
 QY 1005 CGCAGATCCCATGAGAGTGCA 1025  
 Db 241 ArgThrSerHisGlnSerAla 247  
 RESULT 8  
 US-10-372-683-41  
 ; Sequence 41, Application US/10372683  
 ; Publication No. US20040009171A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GERRTSEN, MARY E.  
 ; APPLICANT: PEASE JR., FRANKLIN V.  
 ; APPLICANT: WU, THOMAS D.  
 ; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA  
 ; FILE REFERENCE: P1928R1P1  
 ; CURRENT APPLICATION NUMBER: US/10/372,683  
 ; PRIOR FILING DATE: 2003-02-21  
 ; PRIOR APPLICATION NUMBER: US 10/271,690  
 ; PRIOR FILING DATE: 2002-10-16  
 ; PRIOR APPLICATION NUMBER: US 60/344,534  
 ; PRIOR FILING DATE: 2001-10-18  
 ; NUMBER OF SEQ ID NOS: 49  
 ; SEQ ID NO 41  
 ; LENGTH: 247  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 US-10-372-683-41

Alignment Scores:  
 Pred. No.: 3,97e-106 Length: 247  
 Score: 1268.00 Matches: 247  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 18,56% Indels: 0  
 DB: 15 Gaps: 0

US-09-703-350b-75 (1-3900) x US-10-372-683-41 (1-247)

QY 285 ATGCTCCAAATCAAGAGTGTCTTGTGCTGTGATGATGCTTCTTGCACATGAG 344  
 Db 1 MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20  
 QY 345 GCGAGACAGAAATGACTCTGTGAGCCCGAGAAATCCCGAGTGGCGCTCAAAATCACT 404  
 Db 21 AlaGlnGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnSerAla 40  
 QY 405 GAAAGTGTGCTGCTTCAACAGTGTCTTACAGTGTGGTGGGGGCTTTTCATGCTGTG 464  
 Db 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60  
 QY 465 GAAATCCACCTGACACAGATGGATGTATGACATCTGTAATCCCTTTGTACAGC 524  
 Db 61 GluAsnSerThrCysAspThrAspGlyMetLysPheIleCysLysSerPheLeuYrSer 80  
 QY 525 GCTGCTAAATTTGACACTCAGGAGAAAGATTGCTCAAAAGAGACTTAAATGCATCGCC 584  
 Db 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100  
 QY 585 AACGGGCTACCTCCAGAGTCTTCCGCGCATTCGAGAGTGTCCACTTCCAAAGATG 644  
 Db 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120  
 QY 645 ATTGCTAGAGTGCAGAGAGTGTCTACAGCAAGCTGAATGTGTGACAGATCGCAAGCGG 704  
 Db 121 IleAlaGlnValGlnGlnGlnCysLysSerLysLeuAsnValCysSerIleAlaLysArg 140  
 QY 705 AACCCGTAAGCATCACTGAGTGTGCTGCGCCGCGCATCTTCCAAAGATATCAT 764  
 Db 141 AspProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgLysTyr 160  
 QY 765 AACAGACTGTGCTCGAAGCTGTGTAATGTGATGAAGACACAGTGCAGACATCAGAGAC 824  
 Db 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGlnAspThrValSerThrIleArgAsp 180  
 QY 825 AGCTGTATGAGAAATTTGGGCTTAACATGGCCAGCTTCTTCCAACTCTGACAGCAAC 884  
 Db 181 SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200  
 QY 885 CACTGTGCCCAACACACAGAGTGTCTCAACAGAGAGACCAATAGCCGAG 944  
 Db 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlnProGln 220  
 QY 945 AAGCTGAAGTCTCTCTCGAGAACTCCGAGGTGAGAGAGACTCTTCCCTCCCATCAAA 1004  
 Db 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGlnAspSerProSerHisIleLys 240  
 QY 1005 CGCAGATCCCATGAGAGTGCA 1025  
 Db 241 ArgThrSerHisGlnSerAla 247  
 RESULT 9  
 US-10-614-990-2  
 ; Sequence 2, Application US/10614990  
 ; Publication No. US20040198658A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Olsen et al.  
 ; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods Based Th  
 ; FILE REFERENCE: P108P2  
 ; CURRENT APPLICATION NUMBER: US/10/614,990  
 ; CURRENT FILING DATE: 2003-07-09  
 ; PRIOR APPLICATION NUMBER: US/09/840,989A

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; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-614-990-2

Alignment Scores:
Pred. No.: 3,97e-106 Length: 247
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.56% Indels: 0
DB: 17 Gaps: 0

US-09-703-350b-75 (1-3900) x US-10-614-990-2 (1-247)
QY 285 ATGCTCCAAAGTCAGAGTCTTGTGCTGTGATCAGTCTTGTGCAACCCATGAG 344
DB 1 MetLeuGlnAsnSerAlaValLeuLeuValIleSerAlaSerAlaThrIleGlu 20
QY 345 GCGAGACAGATGACTCTGTGAGCCCGAGAAATCCCGAGTGGCGCTCAAACTCAGCT 404
DB 21 AAGGAGGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
QY 405 GAAGTGTGCTGCTCAGACAGTGTCTACAGGTGCGGTGGGGGCTTTTCATGCTG 464
DB 41 GluValValAlaArgCysLeuAsnSerAlaLeuGlnValIleGlyAlaPheAlaCysLeu 60
QY 465 GAAAGTCACCTGTGACACAGATGGATGATGACATCTGTAATCCTTTGTACAGC 524
DB 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
QY 525 GGTGCTAAATTTGACAGCTCAGAGGAAAGATTCGTCAAGAGAGCTTAAATGCAATGCC 584
DB 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
QY 585 AACGGGTCACCTCCAGGCTCTTCTCCGCAATTCGAGGTGCTCCACTTTCCAAAGATG 644
DB 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
QY 645 ATTGCTGAGGTGACGAGAAAGTGTACAGCAAGCTGAATGTGTGACGATCGCCAAAGCG 704
DB 121 IleAlaGlnValGlnGlnGlnCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
QY 705 AACCCGAGGACATCCTGAGGTGCTGAGGTGCTGAGGTGCTGAGGTGCTGAGGTGCTG 764
DB 141 AsnProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgLysTyr 160
QY 765 AACAGACTTGTCCGAGGCTGCTGAGTGTGATGAAGACAGACAGTCAACAATCAGAGAC 824
DB 161 AsnArgLeuValAlaArgSerLeuGlnCysAspGlnAspThrValSerThrIleArgAsp 180
QY 825 AACCTGATGAGAGAAATTGGGCTTAACATGGGACGCTGCTGCAATCCTGAGAGACAG 884
DB 181 SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
QY 885 CACTGTGCCCAACACACACGAGGCTGACTTCAACAGAGAGACGACCAATGAGCGGAG 944
DB 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlnProGln 220
QY 945 AAGCTGAAGTCTCTCTCAGGAACCTCCAGAGGTGAGAGAGACTTCCCTCCCACTCAA 1004
DB 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGlnAspSerProSerHisIleLys 240
QY 1005 CGCACATCCCATGAGTGA 1025
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DB 241 ArgThrSerHisGlnSerAla 247

RESULT 10
US-09-840-989A-3
; Sequence 3, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stannicalcin Polynucleotides, Polypeptides, and Methods Based The
; FILE REFERENCE: PE108P2
; CURRENT APPLICATION NUMBER: US/09/840,989A
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Oncomyctnus kisutch
; US-09-840-989A-3

Alignment Scores:
Pred. No.: 6,07e-51 Length: 256
Score: 662.50 Matches: 125
Percent Similarity: 73.08% Conservative: 46
Best Local Similarity: 53.42% Mismatches: 54
Query Match: 9.70% Indels: 9
DB: 9 Gaps: 4

US-09-703-350b-75 (1-3900) x US-09-840-989A-3 (1-256)
QY 315 CTGCTGATCAGTGTCTTGTGCAACCCATGAGCGGAGACAGATGACTGTGAGCCGAG 374
DB 12 LeuValLeuGlyThrAlaAlaThrPheAspThrAspProGlnGlnAla---SerProArg 30
QY 375 AAATCCGAGTGGGGGCTCAAAACTCAGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 434
DB 31 ArgAlaArgPheSerSerAsnSerProSerAspValAlaArgCysLeuAsnGlyAlaLeu 50
QY 435 CAGGTGCGTGGCGGGCTTTTGTGATGCTGGAATACTCACTGTGACACAGATGGATG 494
DB 51 AlaValGlyCysGlyThrPheAlaCysLeuGlnAsnSerThrCysAspThrAspGlyMet 70
QY 495 TATGACATCTGTAATCCTTCTGTACAGCGCTGCTAAATTGACACTCAGGGGAAAGCA 554
DB 71 HisAspIleCysGlnLeuPhePheHisThrAlaAlaThrPheAsnThrGlnGlyLysThr 90
QY 555 TTGCTCAAGAGAGCTTAAATGATGATGCCAGCGGGGTCACTCCAGGTCTTCTCGCC 614
DB 91 PheValLysGlnSerLeuArgCysIleAlaAsnGlyValThrSerLysValPheGlnThr 110
QY 615 ATTGGAGGTCTCTCACTTTTCCAAAGATGATGCTGAGGTGACGAGAAAGTGTACAGC 674
DB 111 IleArgArgCysGlyValPheGlnArgMetIleSerIleValGlnGlnGlnCysTyrSer 130
QY 675 AAGCTGATGTGTGACATCGCCAGCGGAGACCTGAAGCATCACTGAGGTGCTCAG 734
DB 131 ArgLeuAspIleCysGlyValAlaArgSerAsnProIleAlaIleGlyGlnValGln 150
QY 735 CTGCCAATCACTTTCACACAGATTAATPACAGACTTGTCCGAGCTGTGGAATGT 794
DB 151 ValProAlaHisPheProAsnArgTyrTyrSerThrLeuGlnSerLeuLeuAlaCys 170
QY 795 GATGAAGACAGACGACCAACATGAGAGACAGACGCTGATGAGAAATTTGGGCTTAACATG 854
DB 171 AspGlnGlnThrValAlaValAlaArgAlaGlyLeuValAlaArgGlyLysProAspMet 190
QY 855 GCCAGCTCTTCCACATCTGTGACAGACAGACACTGTGCCCCAAACACACACGAGCTGAC 914
DB 191 GluThrLeuPheGlnLeuLeuGlnAsnLysHisCysProGlnGlySerAsnGlnGlyPro 210
|||||
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QY 915 TTCAC-----AGAGACGACCAATGAGCCGAGAGCTGAAGTCTC 959  
 Db 211 AanserAlaProAlaIaGlyThraIgrTPrPromeGlySerProPserPheIysIle--- 229  
 QY 960 CTCAGAGACTCCGAGGTGAGAGACTCCCTCCCAATC 1001  
 Db 230 GlnProSerMetArgIlyArgAsp-----ProThrHisLeu 241

# RESULT 11

US-10-614-990-3  
 ; Sequence 3, Application US/10614990  
 ; Publication No. US20040198658A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Olsen et al.  
 ; TITLE OF INVENTION: Stanninocalcin Polynucleotides, Polypeptides, and Methods Based Th  
 ; FILE REFERENCE: PFI08P2  
 ; CURRENT APPLICATION NUMBER: US/10/614,990  
 ; PRIORITY FILING DATE: 2003-07-09  
 ; PRIOR APPLICATION NUMBER: US/09/840,989A  
 ; PRIOR FILING DATE: 2001-04-25  
 ; PRIOR APPLICATION NUMBER: PCT/US00/29432  
 ; PRIOR FILING DATE: 2000-10-26  
 ; PRIOR APPLICATION NUMBER: US 60/161,740  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 256  
 ; TYPE: PRT  
 ; ORGANISM: Oncorhynchus kisutch  
 US-10-614-990-3

## Alignment Scores:

Pred. No.: 6,078-51 Length: 256  
 Score: 662.50 Matches: 125  
 Percent Similarity: 73.08% Conservative: 46  
 Best Local Similarity: 53.42% Mismatches: 54  
 Query Match: 9.70% Indels: 9  
 DB: 17 Gaps: 4

US-09-703-350B-75 (1-3900) x US-10-614-990-3 (1-256)

QY 315 CTGGTATCATGCTCTTCTGCAACCCATGAGCGGAGAGATGACTCTGTGAGCCCAAG 374  
 Db 12 LeuValIleuGlyThrAlaIaIaThrPheAspThrAspProGluIuAla---SerProArg 30  
 QY 375 AAATCCCGAGTGGCGGCTCAAAATCAGCTGAAGTGTCTTGGCTTGAACAGTGTCTTA 434  
 Db 31 ArgAlaArgPheSerSerAsnSerProSerAspValAlaArgCysLeuSngIyAlaLeu 50  
 QY 435 CAGGTGGCTGGCGGCTTTCATGAGCTGGAAGAACTCCACTGTGACACAGATGGATG 494  
 Db 51 AlaValGlyCysGlyIyrPheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMet 70  
 QY 495 TATGACATCTGTAATCTCTTCTTGTACAGCGCTGCTAAATTGACACTCAGGAAAGCA 554  
 Db 71 HisAspIleCysGlnIeuPhePheHisThrAlaAlaIaThrPheAsnThrGlnIyIySthr 90  
 QY 555 TTGCTCAAGAGAGCTTAAATGATGATGATGCTGAGGTGACAGAAAGTGTACAGC 614  
 Db 91 PheValIyGlnIeuSerIeuArgCysIleAlaAsnGlyValIthSerIyValPheGlnThr 110  
 QY 615 ATTGGAGGTGTCTCACTTTCAGAAAGATGATGCTGAGGTGACAGAAAGTGTACAGC 674  
 Db 111 IleArgArgCysGlyIyAlaPheGlnArgMetIleSerGluValGlnIyGlyIySer 130  
 QY 675 AAGCTCAATGTGTGAGCATCGCAAGCGGAGCCCTGAAGCATGACAGAGTGTCTCAG 734  
 Db 131 ArgLeuAspIleIyGlyIyAlaIaArgSerAsnProGluAlaIleGlyGluValAlaGln 150  
 QY 735 CTGCCCAATCACTTCTCCCAAGATACTATAAGACTTGTCCGAGGCTGTGTAATGT 794

Db 151 ValProAlaHisPheProAsnArgIyTyRSerThrLeuIeuGlnIeuIeuAlaCys 170  
 QY 795 GATGACACACAGTACATGACATGACAGCGCTGATGAGAAATTTGGCTTAACATG 854  
 Db 171 AspGlnIuThrValAlaValAlaArgAlaGlyIeuValAlaArgGlnIyProAspMet 190  
 QY 855 GCGAGCTCTTCCACATCCCGACAGACAGACTGTGGCCCAACACACCCAGAGGTGAC 914  
 Db 191 GlnThrIeuPheGlnIeuIeuGlnIeuIyHisCysProGlnIySerAsnGlnIyPro 210  
 QY 915 TTCAC-----AGAGACGACCAATGAGCCGAGAGCTGAAGTCTC 959  
 Db 211 AanserAlaProAlaIaGlyThraIgrTPrPromeGlySerProPserPheIysIle--- 229  
 QY 960 CTCAGAGACTCCGAGGTGAGAGACTCCCTCCCAATC 1001  
 Db 230 GlnProSerMetArgIlyArgAsp-----ProThrHisLeu 241

## RESULT 12

US-10-116-051-10  
 ; Sequence 10, Application US/10116051  
 ; Publication No. US20020146791A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Olsen et al.  
 ; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNILOCALCIN  
 ; FILE REFERENCE: PFI08PIDIC1  
 ; CURRENT APPLICATION NUMBER: US/10/116,051  
 ; PRIORITY FILING DATE: 2002-04-05  
 ; PRIOR APPLICATION NUMBER: 09/312,610  
 ; PRIOR FILING DATE: 1999-05-17  
 ; PRIOR APPLICATION NUMBER: 08/431,117  
 ; PRIOR FILING DATE: 1995-04-28  
 ; PRIOR APPLICATION NUMBER: 08/208,005  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 10  
 ; LENGTH: 204  
 ; TYPE: PRT  
 ; ORGANISM: Oncorhynchus kisutch  
 US-10-116-051-10

## Alignment Scores:

Pred. No.: 8,436-51 Length: 204  
 Score: 660.50 Matches: 118  
 Percent Similarity: 80.41% Conservative: 38  
 Best Local Similarity: 60.82% Mismatches: 37  
 Query Match: 9.67% Indels: 1  
 DB: 13 Gaps: 1

US-09-703-350B-75 (1-3900) x US-10-116-051-10 (1-204)

QY 315 CTGGTATCATGCTCTTCTGCAACCCATGAGCGGAGAGATGACTCTGTGAGCCCAAG 374  
 Db 12 LeuValIleuGlyThrAlaIaIaThrPheAspThrAspProGluIuAla---SerProArg 30  
 QY 375 AAATCCCGAGTGGCGGCTCAAAATCAGCTGAAGTGTCTTGGCTTGAACAGTGTCTTA 434  
 Db 31 ArgAlaArgPheSerSerAsnSerProSerAspValAlaArgCysLeuSngIyAlaLeu 50  
 QY 435 CAGGTGGCTGGCGGCTTTCATGAGCTGGAAGAACTCCACTGTGACACAGATGGATG 494  
 Db 51 AlaValGlyCysGlyIyrPheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMet 70  
 QY 495 TATGACATCTGTAATCTCTTGTACAGCGCTGCTAAATTGACACTCAGGAAAGCA 554  
 Db 71 HisAspIleCysGlnIeuPhePheHisThrAlaAlaIaThrPheAsnThrGlnIyIySthr 90  
 QY 555 TTGCTCAAGAGAGCTTAAATGATGATGATGCTGAGGTGACAGAAAGTGTACAGC 614  
 Db 91 PheValIyGlnIeuSerIeuArgCysIleAlaAsnGlyValIthSerIyValPheGlnThr 110  
 QY 615 ATTGGAGGTGTCTCACTTTCAGAAAGATGATGCTGAGGTGACAGAAAGTGTACAGC 674







GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

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Run on:      November 16, 2004, 08:03:41 ; Search time 125 Seconds
              (without alignments)
              6003.926 Million cell updates/sec
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Perfect score: 6832
Sequence: 1 cagtttgcaaaagccagag.....aaaaaaaaaaaaaaaa 3900
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Ygapop	10.0 , Ygapext 0.5
Fgapop	6.0 , Fgapext 7.0
Delop	6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 5668322

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	45 summaries

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-Q/cgml 1.0/STO pool1 p/USO9703350/runat 16112004 080316 14057/appd_query.fasta_1.40335
-DB-dir 79 -GMMT=fastan -SUFFIX=r3r -MINNAT=0.01 -LOOPC=0 -LOOPEXT=0
-UNITS=51c -START=1 -END=1 -MATRIX=blonum2 -TRANS=numa40.cdi -LIST=45
-LOCALIGN=300 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=DIC NOR=EXC -HEA81SIZE=550 -MINLEN=0 -MAXLEN=2000000000
-USER=US09703350 -CGCN_1 1.194 -errunat 16112004 080316 14057 NCPU=6 -ICPU=3
-NO_MMAP -MARSOSHORT -NGS_SCORES=0 -WAIT -DBSLOC=100 -JONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DEPOP=6 -DELETE=7

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Database :
PIR 79:*
1:  p1r1:*
2:  p1r2:*
3:  p1r3:*
4:  p1r4:*

A>Title: Purification and cloning of a copropuscles of Stenmus protein from Argulilla austr
A:Reference number: A54648; MUID:86083961; PMID:3315739
A:Accession: A54648
A>Status: preliminary
A:Molecule type: mRNA

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## SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	696.5	10.2	263	2	A54648		stannocalcin prec
2	662.5	9.7	256	2	I51197		stannocalcin - cc
3	362	5.3	302	2	JE0357		stannocalcin homo
4	184	2.7	966	2	S25365		CYC8 protein - yea
5	173	2.4	188	2	T15651		hypothetical prote
6	169	2.5	1457	2	T14577		protein kinase Ya
7	168.5	2.4	164	2	T24212		hypothetical prote
8	167.5	2.5	1028	2	A56038		DNA-binding protei
9	164.5	2.4	1403	2	S24538		homeotic protein F
10	163.5	2.4	1213	2	S16356		ovo protein - fru
11	161.5	2.4	286	2	C61615		sericin MG-2 - gre
12	161	2.4	4776	2	E95206		cell wall surface
13	157.5	2.3	539	2	S57912		hypothetical prote
14	156	2.3	1122	2	G64887		probable tail fibe

15	155	2.2	152	2	T18975	hypothetical prote
16	155	2.3	2038	2	A43742	female sterile hom
17	154	2.3	793	2	T46707	proteophosphoglyc
18	153.5	2.2	534	2	T39903	serine-rich protea
19	153.5	2.2	646	2	D82493	conserved hypoten
20	153	2.2	971	2	B90835	probable tail fibre
21	153	2.2	973	2	C85920	probable membrane
22	152.5	2.2	406	2	S31870	SRP40 protein - ye
23	151.5	2.2	356	2	S31574	hypothetical prote
24	151.5	2.2	1032	2	T34343	hypothetical prote
25	151.5	2.2	2150	2	S71629	sensory transducti
26	151.5	2.2	2322	2	T34434	hypothetical prote
27	151	2.2	853	2	T46347	hypothetical prote
28	150.5	2.2	1063	2	D86731	hypothetical prote
29	150	2.2	40	2	B60841	teleocalcin - coho
30	150	2.1	223	2	B38346	ultra-high-sulfur
31	149.5	2.1	220	2	A38346	ultra-high-sulfur
32	149	2.2	40	2	A60841	teleocalcin - sock
33	148.5	2.2	1668	2	T13748	sex comb protein -
34	148	2.2	139	2	A26892	Moba box protein -
35	147.5	2.2	3190	2	T13828	CREB-binding prote
36	147	2.2	653	2	S27770	hypothetical prote
37	146	2.1	1572	2	SNF249A	SNF249A protein
38	145.5	2.1	1708	2	T31095	vitellogenin precu
39	144.5	2.1	730	2	S30543	GLN3 protein - ye
40	144.5	2.1	930	2	T08588	hypothetical prote
41	144.5	2.1	933	3	F86427	auxin response fac
42	143.5	2.1	339	1	TWHU2D	transcription init
43	143.5	2.1	582	2	L47141	gastric mucin (cid
44	143.5	2.1	317	2	T39869	probable lysophos
45	142.5	2.1	796	2	UC7555	Ct4orf4 protein -

## ALIGNMENTS

RESULT 1  
AS4648  
stanniocalcin precursor - Australian eel  
N:Alternate names: stannius corpuscle secretory protein  
C:Species: Anguilla australis (Australian eel)  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2000

R; Butkus, A.; Roche, P.J.; Fentley, R.T.; Harlandbids, J.; Penschow, J.D.; Ryan, G.B.; 1  
Mol. Cell. Endocrinol. 54, 123-133, 1987  
A>Title: Purification and cloning of a corpuscles of Stannius protein from *Anguilla australis*  
A;Reference number: A54648; MUID:88083961; PMID:3319739  
A;Accession: A54648  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-263 <BUT>  
A;Cross-references: UNIPROT:P18301  
F;1-17/Domain: signal sequence #status predicted <SIG>  
F;18-263/Product: stannocalcin #status predicted <MOT>

[illegible]

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Db      40  AspValAlaArgCysLeuSnnIyAlaLeuGlnValGlyCysSerAlaPheAlaCysLeu 59
      465  GAAATCCACCTGTCAGACACAGATGGATGTATGACATCTGTAAATCTTTCTTGACAGC 524
      60  AspAsnSerThrCysAsnThrAspGlyMetH:sgIuIleCysArgSerPheLeuH:sgIy 79
Qy      525  GCTGCTAAATTTGACACTTCAGGAGAAAGATTCGTCGAAGAGAGCTTAAATGCTCCGCC 584
      80  AlaAlaAlaYpAspAspHrInglIyLysHrPheValLysGluSerLeuLysCysH:leAla 99
Db      585  AACGGGTCACCTCCACAGGCTTCTCCGACATTCGAGAGGTGCTCCACTTCCAAAGATG 644
      100  AsnGlyIleThrSerLysValPheLeuThrIleArgArgCysSerSerPheGlnLysMet 119
Qy      645  ATTGCTGAGGTGACGAGAAAGTCTTCACGAAAGCTGATGTGTGACATGCGCAGAGGG 704
      120  IleSerGlnValGlnGlnLysCysLysSerLysLeuAspLeuCysSerValAlaGlnSer 139
Qy      705  AACCCCTGAGCATCTGAGTTCGTCGACGCTCCCAATCACTTCCAAAGATACAT 764
      140  AsnProGlnAlaMetGlyGlnValAlaGlnValProSerGlnPheProAsnArgTyrTyr 159
Db      765  AACACACTTGTCCGAAAGCTGCTGATGTATGAAAGACACAGTCAACATCAGAGAC 824
      160  SerThrLeuLeuGlnSerLeuLeuThrCysAspGlnAspThrValGlnGlnValAlaArgAla 179
Qy      825  AGCCTGATGAGAAATTTGGGCTTAACATGGCCAGGCTCTTCACATCGTCGACAGAC 884
      180  GlyLeuValSerArgLeuGlnProGlnMetGlyValLeuPheGlnLeuGlnThrLys 199
Db      885  CACTGTGCCCAACACACCCACAGAGTGAATTCAACAGAGACGA----- 930
      200  AlaCys-PropSerAlaAlaGlyGlyThrGlyProValGlyAlaGlyLysTyrPar 219
Qy      931  -----CGAATGACCGCGAAGCTGAAAGTCTCTCCAGAAC----- 969
      219  GcysProTyrGlyProProCysSerArgSerSerProThrCysAlaProGlyThrProPr 239
Db      970  -TCCGAGTTCGAGAGAGACTCTCCCTCCCATCAACAGCAGCATCCCATGAGAGT 1023
      239  oThrSerLeuLeuArgAsnAlaArgProAlaProAsnTyrHisProProArgLeu 257

RESULT 2
151197
stanniocalcin - coho salmon
C/Species: Oncorhynchus kisutch (coho salmon)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: I51197
R/Magier, G.F., Dimattia, G.E.; Davie, J.R.; Copp, D.H.; Friesen, H.G.
Mol. Cell. Endocrinol. 90, 7-15, 1992
A/Title: Molecular cloning and cDNA sequence analysis of coho salmon stanniocalcin.
A/Reference number: I51197; MUID:93246046; PMID:1363790
A/Accession: I51197
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-256 <KAG>
A/Cross-references: UNIPROT:Q08264; GB:S59519; NID:g299926; PTDN:AA826419.1; PID:g299927

Alignment Scores:
Pred. No.: 2,98e-46 Length: 256
Score: 662.50 Matches: 125
Percent Similarity: 73.08% Conservative: 46
Best Local Similarity: 53.42% Mismatches: 54
Query Match: 9.70% Indels: 9
DB: 2 Gaps: 4

US-09-703-350b-75 (1-3900) x I51197 (1-256)
Qy      315  CTGGTATACAGGCTCTGCAACCAATGAGGGGAGAGAGAAATGACTGTGTGACCCAGG 374
      12  LeuValLeuGlyThrAlaAlaThrPheAspThrAspProGlnGlnAla---SerProArg 30

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Qy      375  AAATCCGAGTGGGCGGCTCAAAACTCAGCTGAAGTGGTTCGTTGCTCAACAGTGTCTA 434
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Qy      435  CAGTCGCGCTCGGAGGCTTTTGACATCTTGAAATCTCACTGACACAGATGGATG 494
      51  AlaValGlyCysGlyThrPheAlaCysLeuGlnAsnSerThrCysAspThrAspGlyMet 70
Db      495  TATGACATCTGTAAATCTCTTGTACAGGCGCTAAATTTGACACTCAGGAGAAAGCA 554
      71  HisAspIleCysGlnLeuPhePheHisThrAlaAlaThrPheAsnThrGlnGlySerHr 90
Qy      555  TTGCTCAAGAGAGCTTAAATATCATGCGCAAGGAGTCACTCCAAAGTCTTCTCGCC 614
      91  PheValLysGlnSerLeuArgCysIleAlaAsnGlyValThrSerLysValPheGlnThr 110
Db      615  ATTGCGAGGTCTCCACTTTCCAAAGATGATGCTGAGGTGACGAGAAAGTCTACAGC 674
      111  IleArgArgCysGlyValPheGlnArgMetIleSerGlnValGlnGlnGlyCysLysSer 130
Qy      675  AAGCTGATGTGTCAGCATCGCCCAAGCGGAACCTGAAGCATCACTGAGGTGCTCAG 734
      131  ArgLeuAspIleCysGlyValAlaArgSerAsnProGlnAlaIleGlyGlnValGln 150
Db      735  CTGCCCATGACTTTCTCCAAAGATGCTATTAACAGACTGTCCGAAGCTGCTGAAATG 794
      151  ValProAlaHisPheProAsnArgTyrTyrSerThrLeuLeuGlnSerLeuLeuAlaCys 170
Qy      795  GATGAGACAGACTGACCAATCCATCAGAGACAGAGCTGATGAGAAATTTGGCTTAACATG 854
      171  AspGlnGlnThrValAlaValAlaArgAlaGlyLeuValAlaArgLeuGlyProAspMet 190
Db      855  GCCAGCTCTTCACATCTCTGACAGACAGACCACTGTCCCAACACACACAGAGCTGAC 914
      191  GluThrLeuPheGlnLeuLeuGlnMetLysCysProGlnGlySerAsnGlnGlyPro 210
Qy      915  TTGCAC-----AGACAGCCACCAATAGCCCGGAGAGAGTGAAGCTTC 959
      211  AsnSerAlaProAlaGlyTyrArgTyrProMetGlySerProProSerPheLysIle--- 229
Db      960  CTCAGAACCTCCGAGGTGAGAGAGACTCTCCCTCCACATC 1001
      230  GlnProSerMetArgGlyArgAsp-----ProThrHisLeu 241

RESULT 3
JE0357
stanniocalcin homolog - human
N/Alternate names: STC2
C/Species: Homo sapiens (man)
C/Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C/Accession: JE0357
R/Inabaishi, K.; Miyamoto, K.; Takekuni, Y.; Morita, K.; Takeda, E.; Sasaki, S.; Imai, M.
Biochem. Biophys. Res. Commun. 250, 252-258, 1998
A/Title: Molecular cloning of a second human stanniocalcin homologue (STC2).
A/Reference number: JE0357; MUID:98440784; PMID:9753616
A/Accession: JE0357
A/Molecule type: mRNA
A/Residues: 1-302 <ISH>
A/Cross-references: UNIPROT:Q76061; DDBJ:AB012664; NID:g3702223; PTDN:BA33489.1; PID:g3702223
C/Comment: This protein suppressed expression of renal sodium/phosphate cotransporter.
C/Genetics:
A/Introns: 51/1 98/3 169/2

Alignment Scores:
Pred. No.: 1,88e-21 Length: 302
Score: 362.00 Matches: 88
Percent Similarity: 30.00% Conservative: 47
Best Local Similarity: 32.59% Mismatches: 110
Query Match: 5.30% Indels: 25
DB: 2 Gaps: 4

US-09-703-350b-75 (1-3900) x JE0357 (1-302)

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QY	276	TCTCAGAAAGATGCTCAAAATCTCAGACAGTGGCTCTGGTGGTGGTATC-----	323
Db	3	AlaGluArgLeuGluGlnPheMetThrLeuAlaValLeuAlaThrPheAspProAla	22
QY	324	---AGTGGTTCGAACCCATGAGCGGAG---CAGAAATGACTGTGTGAGCCCGAGAA	377
Db	23	ArgGlyThrAspAlaThrAsnProGluGlyProGlnAspArgSerSerGlnGlnGly	42
QY	378	TCCGAGAGGGGGGTCAAAATCTCAGCTGAATGGTCTTGTCCCTCAACAGGCTCTAAG	437
Db	43	GlyArgLeuSerLeuGlnAsnThrAlaGluIleGlnHisCysLeuValAlaAspGlyAsp	62
QY	438	GTCCGGTTCGGGGGCTTTTGACATGCTCGTGAAGAAATCTCACCTGTGACACAGAAAGGATGAT	497
Db	63	ValGlyCysGlyValAlaPheGluCysPheGluAsnAsnSerCysGluAlaArgGlyLeuHis	82
QY	498	GACATCTGTAAATCTTCTTGTACAGCGCTGTAAATTTGACACTCAGCGGAAAAGCATTC	557
Db	83	GlyIleCysMetThrPheLeuHisAsnAlaGlyLysPheAspAlaGlnGlyLysSerPhe	102
QY	558	GTCAAAGAGACATTAATGATCGCCAAACGGGGACCTCCAAAGGTCTTCTCGGCATT	617
Db	103	IleLysAspAlaLeuLysCysLysAlaHisAlaLeuAlaGlnHisArgPheGlyCysIleSer	122
QY	618	CGAAGGTCTCCACTTTTCCAAAGATGATTGCTGAGTGCAGAAAGATGCTACAGCAAG	677
Db	123	ArgLysCysProAlaIleArgGluMetValSerGlnLeuGlnArgGluCysTyrLeuLys	142
QY	678	CTGAATGTGTGAGCATGCGCCAAAGCGGAACCTGAAGCCATCAGAGGTGTCCAGCTG	737
Db	143	HisAspLeuCysAlaAlaAlaIleGlnGluAsnThrArgValIleValAlaMetIleHisPhe	162
QY	738	CCCATCACTTCTCCAAAGATACTATACAGACTTGTGCCAAGGCTGCTGAAATGTAT	797
Db	163	LysAspLeuLeuLeuHisGlnProTyrValAspLeuValAsnLeuLeuMetThrCysGly	182
QY	798	GAAGACAGCTCAGACACATCAGAGACAGCTGATGAGAAATTTGGGCTTAACATGAGCC	857
Db	183	GlnGluValLysGluAlaIleThrHisSerValGlnValGlnCysGlnGlnAsnTrpGly	202
QY	858	AGGCTTTCCACATCTTGGCAG---ACAGACCACTGTGCCCAACACACCCAGAGCTAC	914
Db	203	SerLeuCysSerIleLeuSerPheCysThrSerAlaIleGlnLysProProThrAlaPro	222
QY	915	TTCAACAGAGACCGCACCATGAGCCGCGAGAAGTG-----	950
Db	223	ProGluArgGlnProGlnValAspArgThrLysLeuSerArgAlaHisIleGlyGluAla	242
QY	951	-----AAAGTCTCTCGAGAACCTCCAGAGGTGAGAG	983
Db	243	GlyHisHisLeuProGluProSerSerArgGluThrGlyArgGlyAlaLysGlyGluArg	262
QY	984	GACCTCCCTCCACATCAAAAGCAGCAT	1011
Db	263	GlySerLysSerHis-ProAsnAlaHis	271

RESULT 4  
S25365  
CYC8 protein - yeast (*Saccharomyces cerevisiae*)  
N/Alternate names: glucose repression mediator; protein YB50908; protein YBR112c; SSN6  
C/Species: *Saccharomyces cerevisiae*  
C/Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text change 16-Aug-2004  
C/Accession: S25365; S482777; S45980; S25404; S25405; A30906; S44692  
R/Mannhuapl. G.; Stucka, R.; Ehnlé, S.; Vetter, I.; Feldmann, H.  
Yeast 8, 397-408, 1992  
A/Title: Molecular analysis of yeast chromosome II between CMD1 and LYS2: the excision  
A/Reference number: S25364; MUID:9227848; PMID:1626431  
A/Accession: S25365  
A/Molecule type: DNA  
A/Residues: 1-966 (MAN)  
A/Cross-references: UNIPROT:P14922; EMBL:X66247; NID:q3548; PIDN:CAA6973.1; PID:g3550  
R/Mannhuapl. G.; Stucka, R.; Ehnlé, S.; Vetter, I.; Feldmann, H.  
Yeast 10, 1363-1381, 1994

```

A1Title: Analysis of a 70 kb region on the right arm of Yeast chromosome II.
A1Reference number: S48255; MUID:95508357; PMID:7900426
A1Accession: S48277
A1Status: nucleic acid sequence not shown; translation not shown
A1Molecule type: DNA
A1Residues: 1-966 <MAN>
A1Cross-references: EMBL:X78993; NID:G476045; PIDN:CAAS5615.1; PID:G476068
A1Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
R1Feildmann, H.; Mannheim, G.; Schwarzlöser, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A1Reference number: S45927
A1Accession: S45980
A1Molecule type: DNA
A1Residues: 1-966 <FE2>
A1Cross-references: EMBL:Z35981; NID:G536449; PIDN:CAAS069.1; PID:G536450; MIPS:YBR112c
R1Schultz, J.; Carlson, M.
Mol. Cell. Biol. 7, 3637-3645, 1987
A1Title: Molecular analysis of SSN6, a gene functionally related to the SNF1 protein kinase
A1Reference number: S25404; MUID:88065502; PMID:3316983
A1Accession: S25404
A1Molecule type: DNA
A1Residues: 1-546, 'K', 548-966 <SCH>
A1Cross-references: EMBL:M17826; NID:G172725; PIDN:AAA35103.1; PID:G172726
R1Trimby, R.J.
Gene 73, 97-111, 1988
A1Title: Cloning and characterization of the CYC8 gene mediating glucose repression in yeast
A1Reference number: S25405; MUID:89211964; PMID:2854095
A1Accession: S25405
A1Molecule type: DNA
A1Residues: 1-546, 'K', 548-966 <TRU>
A1Cross-references: EMBL:M23440; NID:G171349; PIDN:AAA34545.1; PID:G171350
C1Genetics:
A1Gene: SGD:CYC8; SSN6; CRT8
A1Cross-references: SGD:S0000316; MIPS:YBR112c
A1Map position: 2R
C1Function:
A1Description: required for complete derepression of ICL1; required for repression of SUC2
C1Superfamily: tetratricopeptide repeat homology
C1Keywords: nucleus; transcription regulation
F1224-257/Domain: tetratricopeptide repeat homology <TT1>
F1263-295/Domain: tetratricopeptide repeat homology <TT2>
F1296-329/Domain: tetratricopeptide repeat homology <TT3>
F1330-363/Domain: tetratricopeptide repeat homology <TT4>
F1365-398/Domain: tetratricopeptide repeat homology <TT5>

Alignment Scores:
Pred. No.: 1.07e-06 Length: 966
Score: 184.00 Matches: 91
Percent Similarity: 39.23% Conservative: 62
Best Local Similarity: 23.33% Mismatches: 136
Query Match: 2.69% Indels: 101
Gaps: 15

```

[illegible]

Db 633 A1aMeGlubHsProlInserSerGlnLeuProProGlnGlnGlnGlnInserVal 652

Qy 213 CAGGAGAGGGAAGGAAAGGGGGGCGAGGAAAAAAACCACCAACTTAGCGGAA 272

Db 653 GlnHsProlGlnInLeuGlnGlnGlnGlnProGlnAlaGlnAlaProlInProLeuIleGln 672

Qy 273 -----ACTCTCAAGAGATGCTCCAAAACCTCAGACAGTGGCTT 308

Db 673 HisAsnValGlnGlnAsnValLeuProGlnIleValSerGlyMetGlnGlnAlaIleHisThr 692

Qy 309 CTGGTGCTGGTGATCAAGTCTTTCGCAACCCATGAGGCGGAGAGATGACTTGAGC 368

Db 693 LeuValAspAlaValSerSerSerThrHis-----ThrGlnAsnThrHisSer 710

Qy 369 CCGAGAGAAATCCCGAATGGCGGCTCAAAACTCAGCTGGAAGTGGTGGCTCCACACAG 428

Db 711 ProArgGln-ProThrHisAlaIleProThrGln----- 721

Qy 429 GCTCTACAGATCGCTCGCGGCTTTTGATCGCTGGAATACTCAGACTGTGACAGAGAT 488

Db 722 -----AlaProAlaThrGlyIleThrAsnAla-----GluProIleValLeuSly 726

Qy 489 GGGATTTATGACACTCTGTAAATCTCTTGTATACAGCGCTGCTAAAT---TTGACACTCAG 545

Db 736 sGlnIleuAsnSerProAsnSeruIleAsnIleValAsnThrAlaThrSerIle 756

Qy 546 GGAAGAGCAATTCGTCAAAGAGAGCTTAAATGATGATCGCA-----AC 587

Db 756 eGluGlnAsnAlaIleValSerGluValSerAsnGlnSerProAlaValValGluSerAsnThr 776

Qy 588 GGGGTCACTCCAGGCTCTTCTCGGCCATTGGAGGTCTCCACTTTCCAAAGAGATGATT 647

Db 776 HisAsnThrSerGlnGlnIleuSlyPro----- 785

Qy 648 GCTGAGGTGAGGAGAGGTGCTACAGAGAGCTGATATGTGCGAGCATGCGCAGCGGAAAC 707

Db 786 -----ValIleSAlaAsnSerIleProSerValIleGlyAlaGlnIleProGlnIle 803

Qy 708 CCTGAAGCCA-----TCACTGAGGTGCTGCACGCTGCCCAATCATCTTCTCCAAAC 755

Db 803 uAlaSerProAlaGluGlnAlaThrHisAlaIleSerValSerProSerThrIleSProle 823

Qy 756 AGATTAATTAACAGACTTGTCGCAAGCTGCTGGATGTGATGAAGACAGTCACAGCAACA 815

Db 823 uAsnThrGlnProGlnSerSer-----SerValGlnProThrValSerSerIle 839

Qy 816 ATCAGAGACAGCCTGATGAGAAATATGGGCTTCAATGAGCGACCTCTTCCACATCTTG 875

Db 839 uSerSerThrThr-----LysHisAsnAspGlnSerThrAlaGlnThrIleGluIle 866

Qy 876 CAGACAGACACTGTGCTCCCAACACACCCACGAGCTGACTTCAACAGAGAGACCCACCAAT 935

Db 856 uSerThrAlaThrValProAlaGlnAla-----SerProVal 868

Qy 936 GAGC-----CGGAGAGAGTGAAGTCCCTCAGAGAACTCCGAGGTGAGAGAGAC 986

Db 868 IgluAspGluValArgGlnHisSerIleSgluGluAsnGlyThrThrGluAla-----Se 886

Qy 987 TCTCCTCCCATCATCAAGCAGCATCC 1014

Db 886 rAlaProSerThrIleGlnIleuPro 895

RESULT 5

T15651

Hypothetical protein C27A2.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence\_rev10 20-Sep-1999 #text\_change 09-Jul-2004

C/Accession: T15651

R.Nhan, M.

submitted to the EMBL Data Library, May 1996

A/Description: The sequence of C. elegans cosmid C27A2.

A/Reference number: Z18382

A/Accession: T15651

```

A:Structure: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-188 <NR>
A:Cross-references: UNIPROT:Q6298; EMBL:U58760; NID:g1330384; PID:g1330389; PIDDN:AAE0077
A:Experimental source: strain Bristol NZ; clone C27A2
C:Genetics:
A:Gene: CBSP.C27A2.5
A:Map position: 2
A:Introns: 19/3; 91/2

Alignment Scores:
Pred. No.: 6.92e-06 Length: 188
Score: 173.00 Matches: 31
Percent Similarity: 48.44% Conservative: 0
Best Local Similarity: 48.44% Mismatches: 17
Query Match: 2.44% Indels: 16
Gaps: 5

US-09-703-350B-75 (1-3900) x T15651 (1-188)
OY TGTCAGCTGCATACACTGAAGAAGCTTAGGTGAGATTGGATGAGATTTTGTGTGTGT 140
Db CGAGGlyGAlYgLYlYgLyglYgLYcysGLy-----cyscys 86
OY 139 TGCTGC-----TGCGATGCTGCTGCTGCCACCCGCTGCTGCTGC-----TGC 92
Db CGcyeyArGProlYscYScycSArGaRgcYcsThCyecyArGrThrcYs 106
OY 91 TGCTCGCCGCGCTGCTGCTGCTGCTGCCACCAGCGCTGCTGCTGC-----TGCTGC 41
Db 107 CyceyeThrArgScYcsThrcYcs--ArGProlYscYcGlyCYsglyCYsgly 125
OY 40 TGCAGTCGCTGC 29
Db 126 cysglycscYcs 129

RESULT 6
T14577
protein kinase Yaka (BC 2.7.1.-) - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T14577
R:Kuspa, A.; Lu, S.; Souza, G.M.
Submitted to the EMBL Data Library, January 1998
A:Description: Yaka, a protein kinase required for the growth to development transition i
A:Reference number: Z18146
A:Accession: T14577
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1457 <KUS>
A:Cross-references: UNIPROT:Q44011; EMBL:AF045453; NID:g2854116; PID:g2854117; PIDDN:AAC07
C:Genetics:
A:Gene: YAKA
A:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein ki

Alignment Scores:
Pred. No.: 1.95e-05 Length: 1457
Score: 169.00 Matches: 103
Percent Similarity: 36.75% Conservative: 69
Best Local Similarity: 22.01% Mismatches: 191
Query Match: 2.47% Indels: 105
Gaps: 14

US-09-703-350B-75 (1-3900) x T14577 (1-1457)
OY 15 CAGAGGTGCAGAGCACTGCAGCAGCAGCAGCAGCAGCGCGCTGTCAGCAGCAG 74
Db 597 Gtnglnclnclnglnclnglnclnglnclnglnclnglnclnglnclnglnclngln 616
OY 75 CACCATGGCGGCAGCAGCAGCAGCAGCAGCGAGGACCCGGTGCACACAGATCACAG 134
Db 617 Gtnglnclnclnglnclnglnclnglnclnglnclnglnclnglnclnglnclngln 636

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QY 135 CAACAACAACAAAAA-----ATCCTCATC 161
Db |||||:::
Db 637 GlnGlnGlnGlnGlnSerSerGlnHisIleGlnIleGlnProLeuGlnLeu 656
QY 162 AAATCCTCACTAGCTTCAAGTATCCAGATCCACATCTCATCTCAACGAGAGAG 221
Db |||||:::
Db 657 PheSerThrProTyrThrSerThrAsnAsnThrProLeuSerSerSerSerSerGly 676
QY 222 GAAAGAGAAAGGGGAGAGAAAAAACCACCAACTTACCGGAAACTTCTCAG 281
Db SerSerLeuAsnAsnLeuLysLysLeuAsnLeuProProPheLysGlnGlnGlnGln 696
QY 282 AGAATG-----CTCCAAAACTCAGCAGTCTT----- 308
Db |||||:::
Db 697 GlnPheSerThrSerGlnAsnSerAspSerPheAsnPheProAsnGlnSerPheSerPro 716
QY 309 -----CTGGTGTCTGTGATCACTGCTTCTGCMAACCCATGAGCGGAGAGATGACTCT 362
Db |||||:::
Db 717 ArgGlyTyrTyrIleProSerSerAlaSerAsnIleGlnGlnGlnGlnProIleAsn 736
QY 363 GTGAGCCCAAGAAATCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGGTTCCTC 422
Db |||||:::
Db 737 IleAsnAsnAsnGlnAsnGlyValGlySerGlnValSer----- 749
QY 423 AACAGTCTCTACAGTCCGGCTTTCATGCTGCTGAAAACCTCCACTGTGAC 482
Db |||||:::
Db 750 GlnLeuAlaLeuGlnSerProSerLeuPheGlyThrProThrAsnIleTyrProPro 769
QY 483 ACAGATGGATGATGATGATCATCTGTAAATCCTTCTGTACAGCGCTGCTAAATTGACACT 542
Db |||||:::
Db 770 TyrSerSerMetCysTyrAsn-----AsenSerProValAlaThrProAsnSerLeuSerPhe 787
QY 543 CAGGGAAGAAACATTCCTCAAGAGAGCTTAAATGATGCCAAGCGGGCTCACTTCCAA 602
Db |||||:::
Db 788 TyrGlySerSerTyrPylSerAspSerSerIleSerLeuAsnProSerThr----- 805
QY 603 GTCCTCTCGCCATTCGGAGGTGCTCCACTTTCMAAGATGATGCTGAGGTGCGAGA 662
Db |||||:::
Db 806 -----ProThrGlnLysGlnMetPhe-----GlnGln 814
QY 663 GAGTGTACAGCAGAGCTGATGTGTGCAGCATCGCAACGAGACCTTGAGCCACTCACT 722
Db |||||:::
Db 815 GlnGlnTyrSerAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnSerAsnAsn 834
QY 723 GAGGTGTCTCAGTGTGCCCACTC-----TCCAAACGATACATATACAGA 770
Db |||||:::
Db 835 AsenAsnGlyAsnAsnThrAsnAsnIleAsnSerAsnAsnAsnAsnAsnValAsnAsn 854
QY 771 CTTGTCCGAGAGCTCTGTGATGTGATGAAGACACAGTCAGCACAATCAGAGAGCCTC 830
Db |||||:::
Db 855 ArgAsnAsnArgSerLysSerAspIleProSerAspSerPheSerSer----- 869
QY 831 ATGGAGAAATTTGGGCTTAACATGCCAGCTTCTTCAATCTCTGAGACACAGACACTGT 890
Db |||||:::
Db 870 SerGlnGlyMetAspProGlnPhe---AsnLeuTyrGlnGlnGlnGlnGlnGln 888
QY 891 GCCCAACACACACCCAGAGCTGACTTCAACAGAGAGACCAACAAATGACCGAGAGACG 950
Db |||||:::
Db 889 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 908
QY 951 AAAGTCTCTCTCAGGAACCTCCGAGGTGAGAGAGACTCTCCTCCCAATCAAAGCACA 1010
Db |||||:::
Db 909 GlnGlnGlnGlnGlnGlnGln----- 916
QY 1011 TCCCATGAGAGTGCATTAACAGGAGAGAGATTATTCACAACTCACCAACTGATTCATT 1070
Db |||||:::
Db 917 -----TyrGlnGlnGlnPheGlnThrLeuGlnAsp 926
QY 1071 TTAGGGGTGTGTGACACACCAATTTGAGTGTACTGTGCTGTTGATTTTAAAGTA 1130
Db |||||:::
Db 927 LeuAsnIleGlnLysLys----- 933
QY 1131 GTTCCATTTTTCATGCC-----CCTTAAAGAAATTTGCAGAACTAGGCTTCTGTAA 1184

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Db 934 ---ProProIleTyrProAsnSerProHisArgLysArgSerHisSer-GlyTyrLeuAs 952
QY 1185 TCAATATCCCAAC-----ATTCCGATGCGACGA 1214
Db |||||:::
Db 952 pGlnTyrAlaAsnGlyTyrAsnSerGlnGlnThrAsnAsnThrGlnGlnGlnGlnGln 972
QY 1215 TTCCCAACCAAAATCCATGATGATCACTTGCCTCTCCAGAGAGAAAGTACCCTTT 1274
Db |||||:::
Db 972 nGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 992
QY 1275 TACCACTTCTCTGCGCATGTC 1296
Db |||||:::
Db 992 pPheSerThrArgMetHisLeu 999

RESULT 7
T24272
hypothetical protein T01B7.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24272
R:Stim, M.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z19667
A:Accession: T24272
A:Status: preliminary; translated from GE/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-164 <WIL>
A:Cross-references: UNIPROT:Q22048; EMBL:Z66499; PID:CAA91301.1; GSPDE:GN00020; CESP:T01
A:Experimental source: clone T01B7
C:Genetics:
A:Gene: CESP:T01B7.8
A:Map position: 2
A:introns: 20/3, 90/2

Alignment Scores:
Pred. No.: 166-05 Length: 164
Score: 168.50 Matches: 33
Percent Similarity: 42.31% Conservative: 0
Best Local Similarity: 42.31% Mismatches: 15
Query Match: 2.38% Indels: 30
DB: 2 Gaps: 5

US-09-703-350b-75 (1-3900) x T24272 (1-164)
QY 199 TGTGATCTGTGATACACTGAAGGCTTGTGAGAGATTGATGAGATTTTGTGTGT 140
Db |||||:::
Db 68 CysGlyCysGly-----CysCys 73
QY 139 TGTGTC-----TGTGATGCTGTGCTGCCACCGATGCTTCGCTGC 98
Db |||||:::
Db 74 GlyCysGlyGlyGlyGlyGlyGlyCysGlyCysCysCysAspPro-----ArgCys 91
QY 97 TGTGCTGCTGCTGCGCGCTGCTGC-----TGTCTGCTGCGACCGCGCTGC 53
Db |||||:::
Db 92 CysCysCysCysAspArgCysCysThrCysCysArgThrCysCysCysThrArgCysCys 111
QY 52 TGTGCTGCTC-----TGTGATGCTGCTGCTTGTGACCTCTGCTTGTGC 7
Db |||||:::
Db 112 ThrCysAspProCysCysCysGlyCys-GlyCysGlyCysGlyCysCys 128

RESULT 8
A56038
DNA-binding protein ovo - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C:Accession: A56038
R:Garfinkel, K.D.; Wang, J.; Liang, Y.; Mahowald, A.P.
Mol. Cell. Biol. 14, 6809-6818, 1994
A:Title: Multiple products from the shavenbaby-ovo gene region of Drosophila melanogaster
A:Reference number: A56038; MUID:95021209; PMID:7935398
A:Accession: A56038
A:Status: preliminary

```

A:Molecule type: mRNA  
A:Residues: 1-1028 <GAR>  
A:Cross-references: UNIPROT:P51521, GB:U1183, NID:G520526, PIDN:AAB60216.1, PID:G520527  
C:Genetics:  
A:Gene: ovo  
;Cross-references: FlyBase:FBgn0003028

Alignment Scores:

Pred. No.:	2,48e+05	Length:	1028
Score:	167.50	Matches:	89
Percent Similarity:	35.50%	Conservative:	42
Best Local Similarity:	24.12%	Mismatches:	114
Query Match:	2.45%	Indels:	124
DB:	2	Gaps:	13

US-09-703-350B-75 (1-3900) X A56038 (1-1028)

[illegible]

QY	645	ATTGCTAGAGTGCAGGAAAGAGTGTCTACAGCAACCTGAATATGTGCAGCATGCGCAAGCGG	704
Db	674	gLyLeuAryGlyAryAlaLysAlaValAlaTyrGlySerThiMetIlethiLeuIleSe	694
QY	705	AACCCCTGAAGCCATCA-----CTGAG	725
Db	694	rThiLeuLysSerSerProGluValProAlaThrLysThrValHisArgThrThiLeuAry	714
QY	726	GTCC-----TCCAGCTCCCAATCACTTGTCCCAACAGATCTAT	764
Db	714	gSerLeuAlaIthiAlaAlaIthiAlaAlaIthiAlaAlaGlyLeuLeuAlaProSerProthiAry	734
QY	765	AACAGACTTGTCCGAAAGCCCTGCAATGTGATGAAAGACACAGCTACAGACACATCAAGAC	824
Db	734	ISeValLeuAsnIleSer-----LysValLeuGln-----	744
QY	825	AGCCTGATGAGAAATTTGGGCTTA	849
Db	745	-----ArgArgLeuGlyLeu	749

## RESULT 5

homeotic protein prospero - fruit fly (*Drosophila melanogaster*)  
C1:Species: *Drosophila melanogaster*  
C1:Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text\_change 09-Jul-2004  
C1:Accession: S24548; J01397; A41089  
R1:Doe, C.Q.  
submitted to the EMBL Data Library, February 1992

A;Reference number: S24548

A:Accession: S24548  
A:Molecule type: DNA  
A:Residues: 1-1403 |DOE|  
A:Cross-references: UNIPROT:P29617; EMBL:Z11743; NID:G8383; PID:G8384  
R:Matsumaki, F., Koltun, K., Hama, C., Yoshiohoka, T., Nakashima, Y.  
Biochem. Biophys. Res. Commun. 182, 1326-1332, 1992  
A:Title: Cloning of the Drosophila prospero gene and its expression in ganglion mother cells  
A:Reference number: J01397; MIMD:Z171948; PMID:1540176

A:Accession: J01397  
A:Molecule type: mRNA  
A:Residues: 1-417, 'Q', 419-1403 <M>  
A:Cross-references: GB:101069; DDBJ:D90560; NID:g217345; PIR:d1001939; PIR:g217346  
A:Vaasson, H.; Geall, E.; Wolff, E.; Blev, E.; Jan, L.Y.; Jan, Y.N.

A:Title: prospero is expressed in neuronal precursors and encodes a nuclear protein that  
A:Reference number: A41089; MUID:92069760; PMID:1720353

A<sub>1</sub> Accession: A41089  
A<sub>1</sub> Molecule type: mRNA

A<sub>1</sub>Residues: 1-75, 'GGDAERAVVPPDEAGGRNEMPA', 99-119, 'NLALQFHVQAAAAAITALLPIG', 145-676, 'C  
A<sub>1</sub>Cross-references: GB:M81389; NID:g158183; PID:g158184

C,Genetics:  
A,Gene: FlyBase:pros

**A:** Cross-references: FlyBase:FBgn0004595  
**C:** Keywords: DNA binding; nucleus; transcription regulation

F.717-734/Region: glutamine-rich  
F.191-998/Region: nuclear location signal

F:1029-1049/Region: glutamine-rich

Alignment Scores:	
Pred. No.:	1403
4.57e-05	length:
1.74 E-05	width:
1.74 E-05	height:

Score:	164.50	Matches:	121
Percent Similarity:	33.27%	Conservative:	61
Percent Identical:	22.10%	Mismatch:	179

Best Local Similarity:	22.126	Mismatches:	1/8
Query Match:	2.418	Indels:	187
	5	Chars:	21

DB: 2      Gdps: 2.1

[illegible][illegible][illegible]

[illegible]

```

QY      930  ACCAATGAGCGCCGACAAAGCTGAAAAGTCTCTCCAGCAACTCCGAGATGAGAGACTCT 989
Db      1067  erGlyGlyAlaIaIaIaYrHsIProGlnIProIProIProIProIProIProIProIProI 1087
QY      990  CCCTCCGCATCAATAAACGACATCCCATGAGAGTGCATAACACGAGGAGGTTATTGACAA 1049
Db      1087  erIePProIhSerValAlaIeIProIaProIaProIaSerLeuHsIgluSerIySvalIphSer- 1106
QY      1050  CCTACCCAACTAGATATCATTTTAAAGGGGTGTTGACACACCAATTTTGAAGTACTGTGCC 1109
Db      1107  ProIyIaSer----- 1109
QY      1110  TGGTTGATATTTTTTAAAGTAGTCTTATTTTCTATCCCTTAAGAAATATGCATGAA 1169
Db      1110  -----ProIhePheaaProHsIaIaIaIaIaIaIa 1121
QY      1170  ACTAGGCTTTGTGTAATCAATATCCCAACTTGTGCATATGAGACATTTCCGACCAACAA 1229
Db      1122  ThrIaIaIaIa-----GlnIeuhIsgIlnHsIhS- GlnGlnHsIhSProHsIhSgInse 1139
QY      1230  TCCATGTATCATCTTGCCTCTCCCTCAGAGAGAAAGTACCTCTTTTACCAACTCTCTG 1289
Db      1139  r---MetGlnIeuhSerSerSerPro-----ProGlySerLeuGlyAlaIeuh 1154
QY      1290  CCATGTCTTTTCCCTGCTCCCTCCCTGAGACCAACCCCAACAAACATTCATGTAACTC 1349
Db      1154  rAsPserIaIaPserProIProIeuhProHsIProIProSerMetLeuHsI----- 1170
QY      1350  TCCAGCCATTGTA 1362
Db      1171  -ProIaIeuh 1174

RESULT 10
S16356
ovo protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Dates: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S16356
R:Mevel-Ninio, M.; Terracol, R.; Kafatos, F.C.
EMBO J. 10, 2258-2266, 1991
A:Title: The ovo gene of Drosophila encodes a zinc finger protein required for female ge
A:Reference number: S16356; MUID:91293102; PMID:1712294
A:Accession: S16356
A:Status: preliminary
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1213 <MEV>
A:Cross-references: UNIPROT:Q8T8L9; EMBL:X59772
C:Gene: FLYBase:OVO
A:Cross-references: FLYBase:FBgn003028
A:Introns: 931/3; 1152/3

Alignment Scores:
Pred. No.: 5 42e-05 Length: 1213
Score: 163.50 Matches: 113
Percent Similarity: 34.76% Conservative: 66
Best Local Similarity: 21.94% Mismatches: 151
Query Match: 2.39% Indels: 185
DB: 2 Gaps: 25

US-09-703-350B-75 (1-3900) x S16356 (1-1213)

QY      24  AAGAAGCAGCCACTGCAGAGACGACGACGACGCGCGGTGGACGACGACGACGAG--- 80
Db      775  gInGlnGlnLeuLeuSerGlnGlnGlnGlnSerHsIhSgInGlnGlnGlnGln 794
QY      81  -----CGCGGACGACGACGACGACG 101
Db      795  GlnHsIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 814
QY      102  CGGAGGACACCGGTGGACGACGAG-----CATCACGACGACACAAACAA 149
Db      102  CGGAGGACACCGGTGGACGACGAG-----CATCACGACGACACAAACAA 149

```



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Db      815 GlnGlnHisHisGlnGlnGlnGlnHisHisSerPheHisHisGlnGlnGlnGln--- 833
QY      150 AAAATCCTGATCAAAATCCTCACTGATTCAGTGTATCCAGATCCAGATCTTCACTCA 209
Db      834 -----ProGlnProGlnSerHisHis 840
QY      210 AGCCAGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 269
      |||
      |||
      |||
Db      841 SerHisHisHisGlnHisGlnHisSerPheHisHisSerSerSerSerSerSerSer 857
QY      270 GAACCTTCTCAGAGATGCTCCAAATCTAGACAGTCTCTGTGTGTGTGTGTGTGTCT 329
      |||
      |||
      |||
Db      858 ProThiAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 877
QY      330 TCTGCACACCCAT-----GAGCGGAGAGAGATGACTGTGTGAGCCCGAGAAA 377
      |||
      |||
      |||
Db      878 AlaAlaAlaHisLeuGlnHisProMetSerSerSerSerSerSerSerSerSerSer 897
QY      378 TCCCGAGTGGCGGCTTAAATCTGAGTGAAGTGTCTGTCTGTCTGTCTGTCTGTCTG 437
      |||
      |||
      |||
Db      898 SerAsnSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 917
QY      438 GTGCGTGTGGCGGCTTGTGATGATGCTGGAATCTGCATCTGTGACAGATGGATGTAT 497
      |||
      |||
      |||
Db      917 GAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 930
QY      498 GACATCTGTAATCTTCTTGTGACAGCGCTGTAATTTGACATCAGAGAGAGAGATTC 557
      |||
      |||
      |||
Db      930 ----- 930
QY      558 GTCAAGAGAGCTTAATATGATTCGCCAAGGGGTCATCCAGATGTTCTTCCGCCATT 617
      |||
      |||
      |||
Db      931 -----SerLeuGlyLeuProProAlaSerLeuGlnLeuGln 942
QY      618 C-----GGAGGT-----GCTCCACTTTCCAAAGATGATGCTGAGGTGAG 659
      |||
      |||
      |||
Db      942 eValaLeuGlnGlyHisGlyHisGlyHisLeuAsnProLeuAla-ValGlnAsnAlaHisGlyGly 962
QY      660 GAAGAGTCTCAAGCAAGCTGAATGTG-----C 689
      |||
      |||
      |||
Db      962 HisHisArgIleArgAsnIleAspCysIleAspAsnSerLeuHisHisHisSerG 982
QY      690 AGCATGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 749
      |||
      |||
      |||
Db      982 LHisGlnGlnGlnGln-----GlySerProGlnGlnGlnAsnMetG 996
QY      750 TCCACAGATCTATTAACAAGCTGTCCAGAGCTGTGGAATG-----TGAT 797
      |||
      |||
      |||
Db      996 LngLiservAlGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1016
QY      798 GAAGACAGAGTCAAGCAATCAAGACAGAGCTGATGAGAAATGGGCTTAACATGGCC 857
      |||
      |||
      |||
Db      1016 LngLHisHisGlnHisHisSerAsnSerSerSerSerSerSerSerSerSerSer 1035
QY      858 AGCCTTTCACACATCTTCGACAGACAGACATGTGCCAAACACACCACGAGCTGACTTC 917
      |||
      |||
      |||
Db      1036 -SerAlaGlnAlaLeuCys-----MetGlySe 1044
QY      918 AACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 966
      |||
      |||
      |||
Db      1044 SerArgGlyGlyAla-----AsnGlnAspSerSerSerSerSerSerSerSerSer 1059
QY      967 -----ACCTCCGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1004
      |||
      |||
      |||
Db      1059 eValCysArgValCysMetLeuThrPheSerLeuGlnArgLeu-----As 1075
QY      1005 CGCACATCTCCATGAGAGGTGATTAACAG-----GAGA 1037
      |||
      |||
      |||
Db      1075 nArgHis--MetLeuHisHisSerAsnSerSerSerSerSerSerSerSerSerSer 1094
QY      1038 GGTATTACCAACCTCAACCAACCTCAATTTAGGGGTGTGACACACCAAT----- 1092
      |||
      |||
      |||
Db      1094 SerGlyPheAsnSerThrPheAspLeuHisArg-----HisThrArgThrHis 1109

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QY      1093 -----TTGAGTGTACTGTGCTGGTGTGATTTTAAAGTAGTGTCT 1136
      |||
      |||
      |||
Db      1109 sThrGlyValArgProGlyThrCysAsn-----LeuCysGlnHisSerHis 1125
QY      1137 ATTTTATGCCCCCTTAAGAAATGTCATGAATAAGCTTGTGTAATCAATGCCAA 1196
      |||
      |||
      |||
Db      1125 rGlnArgCysSerLeuGlnHisHisHisHisCysGlnHisVal-----His 1138
QY      1197 CATTTGCAATGGAGAGATTCACCAACCAACA-----AATCC 1232
      |||
      |||
      |||
Db      1138 sSerValGlnHisGlnThrAlaGlyArgGlyAlaGlyAlaGlyMetLeuValCysGln 1158
QY      1233 ATGTGATCATTTGCTGCTCTCTCTCAAGAGAAAGTACCTTTTAAACAACTTCTC- 1287
      |||
      |||
      |||
Db      1158 uCysGlyHisHisThrCysGlnProGlu-----ValHisThrHisHis 1173
QY      1288 -----TGCCATGTCTTTTCCCTGCTCCCTGAG 1317
      |||
      |||
      |||
Db      1173 uLysAsnAsnHisProPheSerProAlaLeuLeuLys 1185

RESULT 11
C61615
sericin MG-2 - greater wax moth (fragments)
N/Alternate names: silk protein MG-2
C/Species: Galleria mellonella (greater wax moth)
C/Date: 18-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 28-Jul-1995
C/Accession: C61615
R/Zurawec, M.; Sehmal, F.; Scheller, K.; Kumaran, A.K.
Insect Biochem. Mol. Biol. 22, 55-67, 1992
A/Title: Silk gland specific cDNAs from Galleria mellonella L.
A/Reference number: A61615
A/Accession: C61615
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-286 <ZUR>
C/Keywords: tandem repeat

Alignment Scores:
Pred. No.: 6.51e-05 Length: 286
Score: 161.50 Matches: 79
Percent Similarity: 38.79% Conservative: 30
Best Local Similarity: 28.11% Mismatches: 108
Query Match: 2.36% Indels: 64
DB: 2 Gaps: 5

US-09-703-350B-75 (1-3900) x C61615 (1-286)
QY      28 AGCAGCGACTGACAGACAGACAGACAGCGCGGTGGACAGACAGACAGCGCGCGC 87
      |||
      |||
      |||
Db      43 SerSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSerGly 62
QY      88 AGCAGCAGCAGCAGCGGAGCGACCGGTGGACAGACAGATCACCAACCAACCAACA 147
      |||
      |||
      |||
Db      63 SerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 82
QY      148 AAAAATCTCATCAATCTCTCACTTAAGCTTCACTGATTCAGAG----- 193
      |||
      |||
      |||
Db      83 SerGlySerSerSerThrAsnAsnSerSer-glySerSerSerThrAsnAlaSerG 102
QY      194 -----TCCACATC 201
      |||
      |||
      |||
Db      102 ySerSerSerSerAsnAsnThrSerGlySerSerSerThrAsnAsnSerSerGly 122
QY      202 TTCACCTCAACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 261
      |||
      |||
      |||
Db      122 rSerAsnAsnSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 142
QY      262 ACTTAGC-----GAAAATCTTTCAGAGAAATGCTCCAAATCTGACGCTGC 306
      |||
      |||
      |||
Db      142 nSerSerGlySerSerGlyIleGlySerLeuSerAsnSerSerSerSerSerSerSe 162
QY      307 TTTGAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 366

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Db 162 rglnalaaahelalysr-serseSerAngValserAlaaspolysererSers 182

Qy 367 GCCCCAGGAATCCCGAGTGGCGGTCTAAACTGAGCTGAAGTGGTTCCTCAACA 426

Db 182 erseralaserAsnserAlaAlaGlnAsnSerAlaser- 195

Qy 427 GTGCTTACAGAGTGGGTCGGGGCTTTGGATGCTCGAATCCACCTGTGACACAG 486

Db 196 -----SerSerGlnThrIleAsnAla 203

Qy 487 ATGGAGATGATGACATCTGTAATTCCTTGTACAGCGCTGCTAAATTGACACTGAG 546

Db 203 spgIysSerGlnAsnGlnSerSerSerSerSerSerSerAlaAla-----GlnA 219

Qy 547 GAAGAAGCTTGCTGCAAGAAGAGCTTAAATGCAATCGCCAAGGGGGTACCTCCAAAGCT 606

Db 219 snSerAla-ThrArgSerGlnValIleAsnAlaaspIysSerGlnSerSerSer 238

Qy 607 TCCTCGCCATTCGAGAGTGCTCCACTTTCCAAAGAGATGATGCTGAGGTGAGAGAGT 666

Db 239 SerSerSerAlaSerAsn-----GlnAlaSer 247

Qy 667 CCTACAGCACTGAATGTGTGCAGCATCGCCAGCGGAACCTCGAAGCCTACTAGG 726

Db 248 AlathrSerSerSerSerValSerAlaaspIysSerGlnSerSerSerSer 267

Qy 727 TCGTCCAGCTCCCATCTCTCCAAACAGATCAATATAGACTTGTCGGAAGCC 783

Db 268 SerSerSerSerSerSerSerSerSerSerSerSerSerSerSerAla 286

RESULT 12

E95206

cell wall surface anchor family protein [imported] - Streptococcus pneumoniae (strain TIGR4)

C:Species: Streptococcus pneumoniae

C:Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004

C:Accession: E95206

R:Retrelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide, J.D.; Umeyama, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle, A.; Nelson, T.; Hickay, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: E95206

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-4776 <KIR>

A:Cross-references: UNIPROT:Q97P71; GB:AE005672; PIDN:AAK75846.1; PID:G14973269; GSPDB:C: A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SPI772

Alignment Scores:

Prod. No.: 0.000105 Length: 4776

Score: 161.00 Matches: 74

Percent Similarity: 42.43% Conservative: 69

Best Local Similarity: 21.96% Mismatches: 160

Query Match: 2.36% Indels: 34

DB: Gaps: 4

US-09-703-350B-75 (1-3900) x E95206 (1-4776)

Qy 23 CAAAGAGAGGAGCTGAGCAGCAGCAGCAGCGGCGTGGCAGCAGCAGCAGCG 82

Db 2799 GlnserAlaserThrSerAlaserAlaserAlaserThrSerAlaserAlaser 2818

Qy 83 GCGCAGCAGCAGCAGCAGCGGAGCGACCGGTGGCAGCAGCAGCATCCACAAACA 142

Db 2819 ThrSerAlaserAlaserAlaserThrSerAlaserAlaserAlaserThrSerAlaser 2838

Qy 143 ACAAATAATCCCATCAATCCTCACTCAAGTTTCAGTGATCCAGATCCACATCT 202

**Db** 2899 AlaseralaserThserAlaserAlaserThserThserAlaserAlaser 2858  
**Qy** 203 TCACTCAAGCCAGGAGGAAAGGAAAAGGGGGCAGGAAAAAACCACMA 262  
Db 2859 ThserAlaserAlaserThserThserAlaserAlaserThserThser 2878  
Qy 263 CTTAGCGGAATCTTCTCAGAGATGCTCCAAAACACTCAGAGTGCTTCT----- 310  
Db 2879 AlaserThserAlaserGluserlaserThserAlaserAlaserlaserThser 2898  
Qy 311 -----GTGCTGGTGCATCAG 325  
Db 2899 AlaserAlaserAlaserThserAlaserAlaserAlaserThserThserAlaserGlu-Se 2918  
Qy 326 TGCTTTCTGCACCCCATGAGCGCGAGACAGATGACTCTGTGAGGCCACAGAAATCCCAGAT 385  
Db 2918 AlaserThserAlaserAlaserAlaserThserThserAlaserAlaserThse 2938  
Qy 386 GCGCGCTCAAAACTCAGCTGAAAGTGCTTCCTCAACAGTCTCTACAGTCCGCTG 445  
Db 2938 AlaserGluserlaserThserThserAlaserAlaserlaserThserAlaserAla 2958  
Qy 446 CGGGGCTTTTGATGCTGAGAAACCTCCACCTGTGACAGAGATGGATGATACATCTG 505  
Db 2958 erAlaserThserAlaser-----AlaserThserAlaserGluser 2975  
Qy 506 TAAATCCTTTGTGTAACAGCGCTGTAAATTGACACTCAGGAAAGCATTCGTCAAAGA 565  
Db 2975 laserThserAlaserAlaserAlaserThserThserAlaserGluserAlaserThser 2995  
Qy 566 GAGCTTAAATGATACGCGCACAGGGGCTCACCTCCAGAGCTTCCTCGCCATTGGAGGTG 625  
Db 2995 laserAlaserlaserThserAlaserAlaserlaserThserAlaserGluser 3015  
Qy 626 CTCACCTTCCAAAGATGATGTGCTGAGGTGACAGNAGTGTCAAGCAAGCTGATGT 685  
Db 3015 laserThserThser-----AlaserAlaserThserAlase 3029  
Qy 686 GTGACGCTCGCCAGCGGAACCTCGAACCATCTACTAGAGTGTCTCAGTGCCTCATCA 745  
Db 3029 laserAlaserThserAlaserAlaserAlaserlaserlaserlaserlaser 3049  
Qy 746 CTTCTCCACAGATCTATAACACTGTGCGAAGCTGTGCGATGTATGAACAGAC 805  
Db 3049 hrserAlaserGluserlaserThserThserThserAlaserlaserThserAlaserG 3069  
Qy 806 AGTAGACAATCAGACAGACGCTGATGAGAAATGTGGCTTCAATCATGCGACGCTCTT 865  
Db 3069 luserlaserThserlaser-----AlaserAlaserThserAlase 3085  
Qy 866 CCACATCTGAGACAGACACTGTGCCAACACACCCAGAGCTGACTTCAACAGAG 925  
Db 3085 laserAlaserThserAlaserAlaserAlaserThserThserAlaserlaserThser 3105  
Qy 926 ACGACCAATGAGCCGAGAGAGCTGAAGTCTCTCAGAAACCTCC 972  
Db 3105 laserGluserlaserThserAlaserAlaserAlaserlaserThser 3120

RESULT 13  
S57972  
hypothetical protein YDR145w - Yeast (Saccharomyces cerevisiae)  
N/Aternate names: hypothetical protein YD8358.f02  
C/Species: Saccharomyces cerevisiae  
C/Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #ext\_change 09-Jul-2004  
C/Accession: S57972  
R/Murphy, L., Richards, C., Harris, D.  
submitted to the EMBL Data Library, July 1995  
A/Reference number: S57971  
A/Accession: S57972  
A/Molecule type: DNA  
A/Residues: 1-539 <MNR>  
I/Cross-references: UNIPROT:003761; EMBL:Z5046; NID:g899393; PIGN:CAA90368.1; PID:g89935;  
J/Experimental source: strain AB972





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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: November 16, 2004, 06:03:25 ; Search time 694 Seconds

(without alignments) 6466.747 Million cell updates/sec

Title: US-09-703-350B-75

Perfect score: 6832

Sequence: 1 cagcttcgcaaaagccagag.....aaaaaaaaaaaaaaaa 3900

Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 3650362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
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-Q=/cgm2/1/USPTO.spool.p/US09703350/runat.16112004.080315.14046/app.query.fasta\_1.4039  
-DB=UniProt\_02 -GFM=fafastan -SUFFIX=rup -MINMATCH=0.1 -LOOPT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdt -LIST=45  
-DOCALL=GEN=200 -THR\_SCORE=pcr -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFM=pcr -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USRR=US09703350.@CGN.1.1.742.@runat.16112004.080315.14046 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -NAT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

UniProt\_02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1268	18.6	247	1	STC1_HUMAN
2	1234	18.1	247	1	STC1_MOUSE
3	1231	18.0	247	1	STC1_FAT
4	1228	18.0	247	2	Q71UE3
5	1228	18.0	247	2	AAC72394
6	1199	17.5	247	2	Q9N0T1
7	1192.5	17.5	246	2	Q7TNS9
8	851	12.5	253	2	Q6DPI8
9	797	11.7	157	2	Q71UE5
10	797	11.7	157	2	AAC97949
11	780.5	11.4	252	2	Q80015
12	779.5	11.4	252	2	Q80014
13	682	10.0	250	1	STC_ANGAU
14	662.5	9.7	256	1	STC_ONCKT
15	662.5	9.7	256	1	STC_ONCKY
16	654	9.6	249	2	Q6NY18

17	654	9.6	249	2	Q98TB7	Q98TB7 osteoglossin
18	654	9.6	249	2	AAH65540	AAH65540 brachydan
19	653	9.6	249	2	Q6PHV3	Q6PHV3 brachydan
20	653	9.6	249	2	AAH56310	AAH56310 brachydan
21	617	9.0	179	1	STC_ONCKE	P43647 oncorhynchu
22	362	5.3	302	1	STC2_HUMAN	Q76061 homo sapien
23	358	5.2	302	1	STC2_MOUSE	Q97561 macaca name
24	356	5.2	296	1	STC2_MOUSE	Q98452 mus musculu
25	356	5.2	296	2	Q9DC56	Q98452 mus musculu
26	356	5.2	296	2	BAH26849	BAH26849 mus muscu
27	352	5.2	296	1	STC2_RAT	Q970X8 rattus norv
28	186.5	2.7	943	1	Y161_SCHPO	Q8LFG9 schizosacch
29	184.5	2.7	1531	2	Q86GH1	Q86GH1 drosophila
30	184	2.7	966	1	SSN6_YEAST	P14922 saccharomyc
31	182.5	2.7	197	1	STC2_CAVPO	P57675 cavia porce
32	182.5	2.7	669	2	Q7UE67	Q7UE67 rhodopirell
33	182	2.7	1325	2	Q9BKV7	Q9BKV7 leishmania
34	181.5	2.7	1537	2	Q86GH5	Q86GH5 drosophila
35	179.5	2.6	1330	2	Q86GH2	Q86GH2 drosophila
36	178.5	2.6	1329	2	Q75JPO	Q75JPO dictyosteli
37	178.5	2.6	1329	2	AA845395	AA845395 dictyoste
38	178	2.6	374	2	Q75JF9	Q75JF9 dictyosteli
39	178	2.6	374	2	AA838911	AA838911 dictyoste
40	177.5	2.6	602	2	Q86GH6	Q86GH6 drosophila
41	177.5	2.6	791	2	Q756S7	Q756S7 ashbya goos
42	177.5	2.6	791	2	AA852858	AA852858 ashbya go
43	176	2.6	1400	2	Q86AL1	Q86AL1 dictyosteli
44	175.5	2.6	753	2	Q6SPF6	Q6SPF6 debrayomyce
45	174.5	2.6	1323	2	Q75B16	Q75B16 ashbya goos

#### ALIGNMENTS

RESULT 1  
ID STC1\_HUMAN STANDARD; PRT; 247 AA.  
AC P52823;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE stannocalcin 1 precursor (STC-1).  
GN Name=STC1; Synonyms=STC;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=fibrosarcoma, and lung carcinoma;  
RA MEDLINE=96077825; Pubmed=7489828;  
RA Chang A.C.-W., Janost U., Hulsbeek M., de Jong D., Jeffrey K.J.,  
RA Noble J.R., Reddel R.R.;  
RT "A novel human cDNA highly homologous to the fish hormone stannocalcin.";  
RT Mol. Cell. Endocrinol. 112:241-247(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=fetal lung;  
RA MEDLINE=96312491; Pubmed=8700837;  
RA Olsen H.S., Cepeda M.A., Zhang Q.-Q., Rosen C.A., Vozzolo B.L.,  
RA Wagner G.F.;  
RT "Human stannocalcin: a possible hormonal regulator of mineral metabolism.";  
RT Proc. Natl. Acad. Sci. U.S.A. 93:1792-1796(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC Jeffrey K.J., Reddel R.R.;  
RA "Characterization of the human stannocalcin 1 gene.";  
RT Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=colon, kidney, and stomach;  
RA MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.2426038959;

Pred. No.:	2,26-90	Length:	247
Score:	1268.00	Matches:	247
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	18.56%	Indels:	0
DB:	1	Gaps:	0

US-09-703-350B-75 (1-3900) x STC1\_HUMAN (1-247)

QY	285	ATGCTCCAAAACCTGACGAGCTCTTCTGTGCTGTGATGACAGTGTCTTGCACCAACCATGAG	344
Db	1	MetleuGlnAsnSerHisValLeuLeuValLeuValIleSerHisSerHisThrHisGlu	20
QY	345	GGGAGACGAATGACTCTGTGAGGCCACGAAATCCGAGTGGCGGCTTAAAACTCAGCT	404
Db	21	AlaGluGlnAsnAspSerValSerProArgLysSerHisValAlaIleGlnAsnSerHis	40
QY	405	GAAAGGTTTCGTTGCTTAAACAGGCTCTACAGGTGGCGTGGCGGGACTTTTGCATGCTG	464
Db	41	GluValValArgCysLeuAsnSerHisLeuGlnValGlyCysGlyAlaPheHisCysLeu	60
QY	465	GAATACTCACCTGTGACACAGATGGAGTATGACATCTGTAATCCTTCTTGTACAGC	524
Db	61	GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer	80
QY	525	GCTGCTAAATTTGACACCTCAGGAAAGCAATTCGTCAAAGAGGCTTAAATGCAATCCGC	584
Db	81	AlaAlaLysPheAspThrGlnGlyLysAlaPheValIleGlnSerLeuLysCysIleAla	100
QY	585	AACGGGGATCACTCCAGAGTCTTCTCGACATTCGAGAGTGTCCACTTTTCCAAAGATG	644
Db	101	AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet	120
QY	645	ATTGCTGAGTGCAGAAAGAGTGTCTACAGCAAGTGTATGTGTGACGATCCGCAAGCGG	704
Db	121	IleAlaGluValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg	140
QY	705	AACCCGGAAGCCATCAGTGAAGTGTGTGAGTGGTCCCATCACTTCTCCAAACAGATCAT	764
Db	141	AspProGlnAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyr	160
QY	765	AACAGACTGTGTCGAGGCTGTGAAATGTGATGAAGACACACTGACGACCAATCGAGAC	824
Db	161	AsnArgLeuValArgSerLeuLeuGlnCysAspGluAspThrValSerThrIleArgAsp	180
QY	825	AGCTGATGAGAAATTTGGGCTTAACATGGCCAGCCTCTTCCACATCCTGACGACGAC	884
Db	181	SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp	200
QY	885	CACGTGCCCAAAACACACCCACGAGTGACTTCAACGAGACGACCAATGAGCCGACG	944
Db	201	HisCysAlaGlnThrHisIleProArgAlaAspPheAsnArgTyrGlnThrAsnGlnProGln	220
QY	945	AAGCTGAAGTCTCTCTCAAGAACCTCCGAGGTGAGAGGACTCTCCCTCCACATCAAA	1004
Db	221	LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGlnAspSerProSerHisIleLys	240
QY	1005	CGCAGATCCCATGAGAGTGCA	1025
Db	241	ArgThrSerHisGluSerHis	247

RESULT 2  
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ID STC1\_MOUSE STANDARD: PRT: 247 AA.

AC 05s1b3;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DS Stannocalcin 1 precursor (STC-1).  
GN Name:STC1; Synonyms=Stc1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALE/C;  
 RX MEDLINE=97179050; PubMed=9027337;  
 RA Chang A.C.-M., Dunham M.A., Jeffrey K.J., Reddel R.R.;  
 RT "Molecular cloning and characterization of mouse stamniocalcin cDNA.";  
 RL Mol. Cell. Endocrinol. 124:185-187(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Mak S.T., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ussidi T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollath S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey U., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Stimulates renal phosphate reabsorption, and could  
 CC therefore prevent hypocalcemia (By similarity).  
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed in many tissues.  
 CC -1- SIMILARITY: Belongs to the stamniocalcin family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: U47815; AAC00050.1; -.  
 DR EMBL: BC021425; AAH21425.1; -.  
 DR GGD: MGI:109131; Stc1.  
 DR GO: GO:0005615; Cytoplasmic space; IDA.  
 DR InterPro: IPR004978; Stamniocalcin.  
 DR Pfam: PF03298; Stamniocalcin; 1.  
 KW Glycoprotein; Hormone; Signal.  
 FT SIGNAL 1 17 Potential.  
 FT PROPEP 18 33 Potential.  
 FT CHAIN 34 247 Stamniocalcin 1.  
 FT DISULFID 45 59 By similarity.  
 FT DISULFID 54 74 By similarity.  
 FT DISULFID 65 114 By similarity.  
 FT DISULFID 98 128 By similarity.  
 FT DISULFID 135 170 By similarity.  
 FT DISULFID 202 202 Interchain (By similarity).  
 FT CARBOHYD 62 62 N-linked (GlcNAc...).(Potential).  
 SQ SEQUENCE 247 AA; 27480 MW; DAD30D8575A513B CRC64;

## Alignment Scores:

Pred. No.: 1,01e-87 Length: 247  
 Score: 1234.00 Matches: 238  
 Percent Similarity: 98.368 Conservative: 5  
 Best Local Similarity: 98.368 Mismatches: 4  
 Query Match: 18.068 Indels: 0  
 DB: 1 Gaps: 0

US-09-703-350B-75 (1-3900) x STC1\_MOUSE (1-247)  
 QY 285 ATGCTCCAAAACCTGACAGTGTCTTCTGCTGTGTATCACTGCTTCTGCAACCCATGAG 344  
 Db MetLeuGlnAsnSerAlaValIleLeuAlaLeuValIleSerAlaAlaAlaHISGlu 20  
 QY 345 GCGGAGCAGATGACTCTGTGAGGCCCAAGAAACCCGAGTGGGGCTTCAAAATTCAGCT 404  
 Db AlaGlnGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40  
 QY 405 GAAGTGATTCCTGCTCAACAGTGTCTTACAGTCCGCTCGGGGCTTTTGACATGCTGCTG 464  
 Db GluValValAlaGlySerLeuAsnSerAlaLeuGlnAlaGlySerGlyAlaPheAlaCysLeu 60  
 QY 465 GAAATCTCCACTGTGTACACAGATGGATGTATGACATCTGTAAATCTTCTTGTACAGC 524  
 Db GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80  
 QY 525 GCTGCTAATTTGACACTGACAGGAAAGCATTTGCTCAAGAGAGACTTAAATGATGATGCGC 584  
 Db AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100  
 QY 585 AACGGGGTCACTCCCAAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 644  
 Db AsnGlyIleThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120  
 QY 645 ATTGCTGAGGTGACAGAAAGTGTATACAGCAAGTGAATGTGTACAGCATTCGCAAGCGG 704  
 Db IleAlaGlnValGlnGluAspCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140  
 QY 705 AACCTGAGGACCATCACTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 764  
 Db AsnProGlnAlaIleThrGlnValIleGlnLeuProAsnHisPheSerAsnArgTyrTyr 160  
 QY 765 AACGACTTGTCCCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 824  
 Db AsnArgLeuValAlaGlySerLeuGlnCysAspLysPheValSerThrValSerThrIleArgAsp 180  
 QY 825 AGCTGTGAGGAAATTTGGGCTTCAACATGAGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 884  
 Db SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200  
 QY 885 CACTGTGCCCAACACACCCACGAGCTGACTTCAACAGGAGCAGCACCACCAATGAGCCGAC 944  
 Db HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlnProGln 220  
 QY 945 AAGCTGAAGTCCCTCCAGGAACCTCCGAGGTGAGGAGGAGTCTCCCTCCCATCATCAA 1004  
 Db LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnLysAspSerProSerHisIleLys 240  
 QY 1005 CGCAATCCCATGAGAGTGA 1025  
 Db 241 ArgThrSerGlnGlnSerAla 247  
 RESULT 3  
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 AC P97574;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE Stamniocalcin 1 precursor (STC-1).  
 GN Name=Stc1; Synonyms=Stc;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;  
 RA Abe T., Tanemoto M., Hall A.E., Brown E.M., Hebert S.C.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Stimulates renal phosphate reabsorption, and could

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CC      therefore prevent hypercalcemia (By similarity).
CC      -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- SIMILARITY: Belongs to the stanniocalcin family.
CC
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL: U62667; AAB39541.1; -.
CC      DR      RGD: 621776; Stcl.
CC      DR      InterPro: IPR004978; Stanniocalcin.
CC      DR      Pfam: PF03298; Stanniocalcin; 1.
CC      KW      Glycoprotein; Hormone; Signal.
CC      FT      SIGNAL      1      17      Potential.
CC      FT      PROPEP      18      33      Potential.
CC      FT      CHAIN      34      247      Stanniocalcin 1.
CC      FT      DISULFID      45      59      By similarity.
CC      FT      DISULFID      54      74      By similarity.
CC      FT      DISULFID      65      114      By similarity.
CC      FT      DISULFID      98      128      By similarity.
CC      FT      DISULFID      135      170      By similarity.
CC      FT      DISULFID      202      202      Interchain (By similarity).
CC      FT      CARBOHYD      62      62      N-linked (GlcNAc...) (Potential).
CC      SQ      SEQUENCE      247 AA; 27507 MW; DAC2FDD8575A513B CRC64;
CC
CC      Alignment Scores:
CC      Pred. No.:      1,74e-87      Length:      247
CC      Score:      1231.00      Matches:      237
CC      Percent Similarity:      98.38%      Conservative:      6
CC      Best Local Similarity:      95.95%      Mismatches:      4
CC      Query Match:      18.02%      Indels:      0
CC      Gaps:      0
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US-09-703-350b-75 (1-3900) x STCL_RAT (1-247)
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QY      285  ATGCTCCAAACTCAGACAGTCTTGTGCTGCTGATCATGCTTTCGCAACCATGAG 344
DB      1  MetLeuGlnAsnSerAlaValIleLeuAlaLeuValIleSerAlaAlaIleAsnGlu 20
CC
QY      345  GCGGAGCAGATGACCTCTGTGAGCCCGAGAAATCCGAGGCGCTCAAAATCAGCT 404
DB      21  AlaGluGlnAsnSerValSerProArgLysSerArgValAlaIleGlnAsnSerAla 40
CC
QY      405  GAATGCTTCGTTGCTCTCAACAGTGTCTTACAGTCTGCGGCTGGGCGCTTTTGATGCTG 464
DB      41  GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
CC
QY      465  GAAAACTCCACTGTGACACAGATGGATGTATGACATCTGTAATCCTTCTGTACAGC 524
DB      61  GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
CC
QY      525  GCTGCTAAATTGACACTCAGGAGAAAGCATTCGTCAAGAGAGCTTAAATGCAATCGCC 584
DB      81  AlaIleAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
CC
QY      585  AACGGGCTCACTCCAAAGCTTTCTCTCGCATTCGAGAGTCTCCACTTTCCAAAGATG 644
DB      101  AsnGlyIleThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgPheC 120
CC
QY      645  ATGTCGAGAGTGCAGAGAGTGCCTACAGCAAGCTGAATGTGTGACAGTCCCAAGCGG 704
DB      121  IleAlaGluValGlnIleLysPheCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
CC
QY      705  AACCTGAAAGCATCTAGAGTGTCTCAGCTGCGCCCAATCACTTCTCCACGATACAT 764
DB      141  AsnProGluAlaIleThrGlnValIleGlnLeuProAsnIlePheSerAsnArgTyrTyr 160
CC
QY      765  AACGACTTGTCCGAGAGCTGTCTGGAATGTATGAAGAACAAGTACGACCAATCAGAGAC 824

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DB      161  AsnArgLeuValArgSerLeuGlnGlyCysAspGluAspThrValSerThrIleLeuAsp 180
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DB      181  SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
CC
QY      885  CACTGTGCCCAACACACCCACGAGCTGACTTTCACAGAGACGACCAATGATGCGCGAG 944
DB      201  HisCysAlaGlnThrIleProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
CC
QY      945  AAGCTGAAGTCTCTCTCAGGAACCTCCGAGGTGAGAGAGACTTCTCCACATCAAA 1004
DB      221  LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGlyLysSerProSerHisIleLys 240
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QY      1005  CGACATCCCATGAGAGTGC 1025
DB      241  ArgThrSerGlnGlnAsnAla 247
CC
RESULT 4
ID      Q71UE3      PRELIMINARY;      PRT;      247 AA.
ID      Q71UE3
AC      05-JUN-2004 (TREMBLrel. 27, Created)
DT      05-JUN-2004 (TREMBLrel. 27, Last sequence update)
DE      05-JUN-2004 (TREMBLrel. 27, Last annotation update)
DE      Stanniocalcin (Mouse).
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Varghese R., Wong C.K.C., Doel H., Wagner G.F., DiMatteo G.E.;
RT      "Comparative Analysis of Mammalian Stanniocalcin Genes.";
RL      Endocrinology 139:4717-4725(1998).
DR      EMBL; AF093098; AAC72394.1; -.
DR      GO; GO:0005615; Cytoplasmic space; IDA.
DR      InterPro: IPR000719; Prot. Kinase.
DR      InterPro: IPR004978; Stanniocalcin.
DR      Pfam: PF03298; Stanniocalcin; 1.
DR      PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.
SQ      SEQUENCE      247 AA; 27495 MW; CA2DEB859BAACB CRC64;
CC
CC      Alignment Scores:
CC      Pred. No.:      2.99e-87      Length:      247
CC      Score:      1228.00      Matches:      237
CC      Percent Similarity:      97.98%      Conservative:      5
CC      Best Local Similarity:      95.95%      Mismatches:      0
CC      Query Match:      17.97%      Indels:      0
CC      Gaps:      0
CC
US-09-703-350b-75 (1-3900) x Q71UE3 (1-247)
CC
QY      285  ATGCTCCAAACTCAGACAGTCTTGTGCTGCTGATCATGCTTCTGCAACCATGAG 344
DB      1  MetLeuGlnAsnSerAlaValIleLeuAlaLeuValIleSerAlaAlaIleAsnGlu 20
CC
QY      345  GCGGAGCAGATGACCTCTGTGAGCCCGAGAAATCCGAGTGCAGGCTCAAAATCAGCT 404
DB      21  AlaGluGlnAsnSerValSerProArgLysSerArgValAlaIleGlnAsnSerAla 40
CC
QY      405  GAATGCTTCGTTGCTCTCAACAGTGTCTTACAGTCTGCGGCTGGGCGCTTTTGATGCTG 464
DB      41  GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
CC
QY      465  GAAAACTCCACTGTGACACAGATGGATGTATGACATCTGTAATCCTTCTGTACAGC 524
DB      61  GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
CC
QY      525  GCTGCTAAATTGACACTCAGGAGAAAGCATTCGTCAAGAGCTTAAATGCAATCGCC 584
DB      81  AlaIleAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100

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QY 585 AACGGGTCACCTCCAGAGTCTTCTGCGCATTCGAGGAGGCTCCACTTTCCAAAGGAG 644
DB 101 AAGGlyIlethrserysValPheleuValIleArgArgCysSerThrPheGlnArgMet 120
QY 645 ATTGCTAGGTGAGAGAGAGTGTCTACAGCAAGCTGATGTGTGACATGCGCAAGCGG 704
DB 121 IleAlaGluValGlnGlnuspCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
QY 705 AACCTGAAGCCATCTCATCTGAGTGTCTCCAGCTGCCAATCACTTCTCCACAGATCTAT 764
DB 141 AsnProGlnAlaIleThrGluValIleGlnGlnProAsnHisPheSerAsnArgTyrTyr 160
QY 765 AACAGACTGTGCGAAGCTGAGTGTGATGTGAGACACAGTGCAGCAATCGAGAGC 824
DB 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
QY 825 AGCTGATGAGAGAAATTGGGCTTAACATGGCCAGCTCTTCCACATCTCTGACAGAC 884
DB 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
QY 885 CACTGTGCCCAACACACCCAGAGCTGACTTCAACAGAGAGACGCAATAGCGCGAG 944
DB 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
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QY 1005 CGCACATCCCATGAGAGTGCA 1025
DB 241 ArgThrSerGlnGlnuSerAla 247

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ID AAC72394 PRELIMINARY; PRT; 247 AA.
AC AAC72394;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DE 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE Stanniocalcin precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Varghese R., Wong C.K.C., Doel H., Wagner G.F., Dimattia G.E.;
RT "Comparative Analysis of Mammalian Stanniocalcin Genes.";
DR EMBL; AF090906; AAC72394.1; -.
SQ SEQUENCE 247 AA; 27495 MW; CA2DEB659BAAFCB CRC64;

Alignment Scores:
Pred. No.: 2,99e-87 Length: 247
Score: 1228.00 Matches: 237
Percent Similarity: 97.98% Conservative: 5
Best Local Similarity: 95.95% Mismatches: 5
Query Match: 17.97% Indels: 0
DB: Gaps: 0

US-09-703-350b-75 (1-3900) x AAC72394 (1-247)
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DB 1 MetLeuGlnAsnSerValIleValIleuValIleSerValAlaAlaIleGlu 20
QY 345 GCGAGACAGAAAGACTCTGTGAGCCCGAGGAATCCGAGTGGCGGCTCAAAATCCAGCT 404
DB 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerVal 40
QY 405 GAAGTGTCTGCTTCTCTCAACAGTGTCTTCAAGTGTGCTGCGGAGCTTTGCATGCTGTG 464

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DB 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
QY 465 GAAAACTCCACCTGTGACACAGATGGATGTATGACATCTGTAATCTTTGTACAGC 524
DB 61 GluAsnSerThrCysAspThrAspGlyMetCysAspIleCysLysSerPheLeuTyrSer 80
QY 525 GCTGTAAATTTGACACTCAGAGAAAGCAATTCGTCAAAGAGACTTAAATGATCGGCC 584
DB 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
QY 585 AACGGGTACCTCCAAAGTCTTCTCGCAATTGAGAGTGTCTCACTTCCAAAGAGTG 644
DB 101 AAGGlyIlethrserysValPheleuValIleArgArgCysSerThrPheGlnArgMet 120
QY 645 ATTGCTAGGTGAGAGAGTGTCTACAGCAAGCTGATGTGTGACATGCGCAAGCGG 704
DB 121 IleAlaGluValGlnGlnuspCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
QY 705 AACCTGAAGCCATCTCATCTGAGTGTCTCCAGCTGCCAATCACTTCTCCACAGATCTAT 764
DB 141 AsnProGlnAlaIleThrGluValIleGlnGlnProAsnHisPheSerAsnArgTyrTyr 160
QY 765 AACGACTTGTCCGAGAGCTGTGGAATGTGATGAGACACAGTGCAGCAATCGAGAGC 824
DB 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
QY 825 AGCTGATGAGAGAAATTGGGCTTAACATGGCCAGCTCTTCCACATCTCTGACAGAC 884
DB 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
QY 885 CACTGTGCCCAACACACCCAGAGCTGACTTCAACAGAGAGACGCAATAGCGCGAG 944
DB 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
QY 945 AAGCTGAAAGTCTCTCTCCAGAACTCCGAGGTGAGAGAGACTTCTCCCTCCACATCAA 1004
DB 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGlyAspSerProSerHisIleLys 240
QY 1005 CGCACATCCCATGAGAGTGCA 1025
DB 241 ArgThrSerGlnGlnuSerAla 247

RESULT 6
ID Q9NOT1 PRELIMINARY; PRT; 247 AA.
AC Q9NOT1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Stanniocalcin.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Ovary;
RA Dimattia G.E.;
RL EMBL; AF257506; AAF68996.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin.1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN.1.
SQ SEQUENCE 247 AA; 27555 MW; F5942A715E2A3JED0 CRC64;

Alignment Scores:
Pred. No.: 5.61e-85 Length: 247
Score: 1199.00 Matches: 234
Percent Similarity: 96.76% Conservative: 5

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ID 06DF18 PRELIMINARY; PRT; 253 AA.
AC 06DF18;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=6355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wak S.T., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman W., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.J., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research. The NIH Xenopus
RT Initiative."
RT Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Strausberg R.,
RT Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076749; AAH76749.1; -
KW Hypothetical protein.
SQ SEQUENCE 253 AA; 28127 MW; DFC93366DA31765D CRC64;

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DB 52 LeuansnglyalaleuGlnValGlyCysGlyAlaIlePheAlaCysLeuGlnuSerThrThrCys 71
QY 480 GACACAGATGGAGTGTATGACATCTGTAATCCCTTCTGTACAGCGGTCTTAATTTGAC 539
DB 72 AsphthrasgilyleuTyrrAspIleCysAlaIlePheAlaIlePheAlaIlePheAsp 91
QY 540 ACTCAGGAAAGAGATTCGTCAAGAGAGAGCTTAAATGATCGGCAACGGGGTCCCTCC 599
DB 92 ThrGlnGlyValPheValIleGlySerLeuGlnuSerLeuGlnuSerLeuGlnuSer 111
QY 600 AAGCTCTCCCTCCGATTCGAGAGGTCTCCATCTTCCAAAGATGATTCGTGAGTCCAG 659
DB 112 LysValPheLeuSerIleValGlyArgCysSerSerGlnGlnuSerGlnuSerGlnuValGln 131
QY 660 GAAGAGTGTCTACAGACAGTGAATGTGTGACATCCGACCAAGCGGAGACCTGAGGCATC 719
DB 132 GlnAspCysTyrrThrIleValMetAspIleCysThrValAlaGlnuTyrrAsnProAspAlaIle 151
QY 720 ACTGAGTGTCTCCAGCTCCCATCATCTTCTCCACAGATTAATTAACAGACTTGTCCGA 779
DB 152 ThrGlnuValAlaIleValPheGlnuSerIlePheSerAsnArgTyrrAsnThrLeuValArg 171
QY 780 AGCGTGTGATGTGATGTAAGACACAGATGACACATCCAGACAGACAGCTGATGAGAA 839
DB 172 SerLeuLeuAspCysAspGlnuThrValSerIleValIleValIleValIleValIleVal 191
QY 840 ATTGGGCTTAATGATGGCCAGCTCTTCCACATCTGTCAGACAGACCACTGTGCCAACA 899
DB 192 IleGlyProAlaIleValIleSerLeuPheGlnuValIleGlnuGlnuValIleGlnuIle 211
QY 900 CACCCAGAGGTGCTTCCACAGAGACAGACCAATGAGCGGAGAGCTGGAAGTCTC 959
DB 212 GlnProArgMetCysAspPheAsnArgIleValIleAsnIleAspProGlnuValIleValIle 231
QY 960 CTCAGAACCTCCGAGGTGAGAGACTCT 989
DB 232 LeuArgAsnLeuArgGlyGlnuSerSer 241

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RESULT 9

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ID Q71UE5 PRELIMINARY; PRT; 157 AA.
AC Q71UE5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Stanniocalcin (Fragment).
GN Name=STC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99008615; PubMed=9794484;
RA Varghese R., Wong C.K., Deol H., Wagner G.F., DiMatteo G.E.;
RT "Comparative analysis of mammalian stanniocalcin genes."
RL Endocrinology 139:4714-4725 (1998).
DR EMBL; AF098463; AAC97949.1; -
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
FT NON TER 157
SQ SEQUENCE 157 AA; 17094 MW; E22F2A6067966C3E CRC64;

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Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
1.62e-53	157	157	157	0	0	0
Percent Similarity:	797.00	100.00%	100.00%	0	0	0
Best Local Similarity:	100.00%	100.00%	100.00%	0	0	0
Query Match:	11.67%	11.67%	11.67%	0	0	0

US-09-703-350B-75 (1-3900) x Q71UB5 (1-157)

```

QY 285 ATGCTCCAAACTCAGCAGTCTTGTGCTGATGATGCTTTGCAACCATGAG 344
   |||||
Db 1 MetLeuGlnAsnSerValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
QY 345 GCGGAGCAAAAGACTCTGTGAGCCCGGAAATCCGAGGCGGCTCAAACTCAGCT 404
   |||||
Db 21 AlaGlnGlnAsnSerValSerProAlaGlySerValAlaAlaGlnAsnSerAla 40
QY 405 GAAGTGTTGCTGCTCAACAGTCTTACAGTCCGCTGCGGGCTTTTGATGCTG 464
   |||||
Db 41 GluValValArgCysLeuAsnSerValLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
QY 465 GAAACTCCACTGTGACACAGATGGAGTATGACATCTGAAATCCTTCTTGACAGC 524
   |||||
Db 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
QY 525 GCTGCTAAATTGACACTCAGGAGAAAGCATTCGTCAAGAGAGCTTAAATGATCGCC 584
   |||||
Db 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
QY 585 AACGGGCTACCTCCCAAGGCTTCTTCCGCAATTCGAGGCTCTCCACTTTCCAAAGATG 644
   |||||
Db 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
QY 645 ATGTGCTGAGTGAGGAGAGAGTGTCTACAGCAAGTGAATGTGACGATCGCCAGGCG 704
   |||||
Db 121 IleAlaGlnValAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 140
QY 705 AACCTGGAAGCATCATCTGAGGCTCGTCAGCTGCCCATCTTCTCCAAAC 755
   |||||
Db 141 AsnProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsn 157

RESULT 10
AAC97949 PRELIMINARY; PRT; 157 AA.
ID AAC97949;
AC AAC97949;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DB Stannicalcin (Fragment).
GN STC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9008615; PubMed=9794484;
RA Varghese R., Wong C.K., Deol H., Wagner G.F., Dimattia G.E.;
RT "Comparative analysis of mammalian stannicalcin genes.";
RL Endocrinology 139:4714-4725(1998).
DR EMBL; AF098463; AAC97949.1; -.
FT NON TER 157
SQ SEQUENCE 157 AA; 17094 MW; E22P2A6067966C3E CRC64;

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Alignment Scores:

Pred. No.:	Length:	Score:
1.62e-53	157	797.00
Percent Similarity:	Matches:	157
100.00%	Conservative:	0
Best Local Similarity:	Mismatches:	0
11.67%	Indels:	0
Query Match:	Gaps:	0

US-09-703-350B-75 (1-3900) x AAC97949 (1-157)

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QY 285 ATGCTCCAAACTCAGCAGTCTTGTGCTGATGATGCTTTGCAACCATGAG 344
   |||||
Db 1 MetLeuGlnAsnSerValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
QY 345 GCGGAGCAAAAGACTCTGTGAGCCCGGAAATCCGAGGCGGCTCAAACTCAGCT 404
   |||||

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Db 21 AlaGlnGlnAsnSerValSerProAlaGlySerArgValAlaAlaGlnAsnSerAla 40
QY 405 GAAGTGTTGCTGCTCAACAGTCTTACAGTCCGCTGCGGGCTTTTGATGCTG 464
   |||||
Db 41 GluValValArgCysLeuAsnSerValLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
QY 465 GAAACTCCACTGTGACACAGATGGAGTATGACATCTGAAATCCTTCTTGACAGC 524
   |||||
Db 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
QY 525 GCTGCTAAATTGACACTCAGGAGAAAGCATTCGTCAAGAGAGCTTAAATGATCGCC 584
   |||||
Db 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
QY 585 AACGGGCTACCTCCCAAGGCTTCTTCCGCAATTCGAGGCTCTCCACTTTCCAAAGATG 644
   |||||
Db 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
QY 645 ATGTGCTGAGTGAGGAGAGTGTCTACAGCAAGTGAATGTGACGATCGCCAGGCG 704
   |||||
Db 121 IleAlaGlnValAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 140
QY 705 AACCTGGAAGCATCATCTGAGGCTCGTCAGCTGCCCATCTTCTCCAAAC 755
   |||||
Db 141 AsnProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsn 157

```

```

RESULT 11
Q80015 PRELIMINARY; PRT; 252 AA.
ID Q80015;
AC Q80015;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DB Stannicalcin precursor.
GN Name=STC;
OS Amia calva (Bowfin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Amniformes; Amniidae; Amia.
OX NCBI_TaxID=7924;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14697312;
RA Amemiya Y., Youson J.H.;
RT "Primary structure of stannicalcin in two basal Actinopterygii.";
RL Gen. Comp. Endocrinol. 135:250-257(2004).
DR EMBL; AB106622; BAC66163.1; -.
DR GO; GO:0005176; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR000719; P:prot kinase.
DR InterPro; IPR004978; Stannicalcin.
DR Pfam; PF03298; Stannicalcin; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
KM SIGNAL.
FT SIGNAL 1
FT CHAIN 33
FT CHAIN 252
SQ SEQUENCE 252 AA; 27868 MW; B9D9663610DF0B5D CRC64;

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Alignment Scores:

Pred. No.:	Length:	Score:
3.54e-52	252	780.50
Percent Similarity:	Matches:	145
85.19%	Conservative:	39
Best Local Similarity:	Mismatches:	30
67.13%	Indels:	2
Query Match:	Gaps:	1

US-09-703-350B-75 (1-3900) x Q80015 (1-252)

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QY 285 ATGCTCCAAACTCAGCAGTCTTGTGCTGATGATGCTTTGCAACCATGAG 344
   |||||
Db 1 MetLeuGlnAsnSerValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
QY 345 GCGGAGCAAAAGACTCTGTGAGCCCGGAAATCCGAGGCGGCTCAAACTCAGCT 404
   |||||

```

Db	20	LeuAspGlnAsnGluSerPheSerProArgAArgTrnArgValSerAlaHisSerSer	39
Qy	405	GAAGTGGTTCGTGGCTTCAACAGTGTCTACAGGTCGGCTGGGGGCTTTGGCATGCTTG	464
Db	40	AspValAlaArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu	59
Qy	465	GAAGATCCACCGTGCACACAGATGGGATGTATGATCTCTAAATCCTTCTTGAAGC	524
Db	60	GluAsnSerThrCysAspThrAspGlyMetHisAspIleCysGlySerPheLeuThrSer	79
Qy	525	GCTGCTAAATTGACACTCAGGAGAAAGCATTGCTCAAGAGAGCTTAAATGCAATGCC	584
Db	80	AlaAlaIysPheAspThrGlnGlySerValAPheValIysGluSerLeuIysCysIleAla	99
Qy	585	AAGGGGGATCACCCGCAAGGCTTCCTCCGCGCATTCGGAGAGTGTCTCACTTCCAAAGATG	644
Db	100	AsnGlyIleHisSerIysValPheLeuThrIleAsnArgCysSerThrPheGlnArgMet	119
Qy	645	ATTGCTGAGGTGCAGGAGAAGAGTGTCTACAGCAAGCTAAATGTGTACAGATGCCACGG	704
Db	120	IlleSerGluValAlaGlnGluGlyCysThrThrIysLeuAspIleCysGluValAlaArgLeu	139
Qy	705	AACCTGAAAGCCATCATCTGAGGTTCGTCAGCTGCCCATTCATCTTCTCCACAGATACTAT	764
Db	140	AspProGluAlaIleSerGluValAlaGlnLeuProSerHisPheProAsnArgTyrTyr	159
Qy	765	AACAGACTGTCCGAAGCTGCTGATGATGTATGAAACAGACATCAGACATCAGAGAC	824
Db	160	SerIysLeuLeuGlnSerLeuMetGluCysAspGlnGluThrIvalSerValAlaArgSer	179
Qy	825	AGCCTATGAGCAAAATTGGGCTTACATGCGCAGCTCTTCCACATCTTCGACACAGAC	884
Db	180	AsnLeuValSerArgPheGluPyrGluMetSerMetLeuPheGlnLeuGlnSerIys	199
Qy	885	CACGTGCCCCAAACACAGCCACGAGGTGACTTCAACAGAGACGCA	930
Db	200	ProCys-ProAlaSerSerAlaSerSerThrSerSerAlaGlyAla	214
RESULT 12			
Q880014			
ID	Q880014	PRELIMINARY;	PRT; 252 AA.
AC	Q880014;		
DT	01-JUN-2003 (T-EMBLrel. 24, Created)		
PT	01-JUN-2003 (T-EMBLrel. 24, Last sequence update)		
DT	01-MAR-2004 (T-EMBLrel. 26, Last annotation update)		
DE	Stanniocalcin precursor.		
GN	Name=STC;		
OS	Lepisosteus osseus (Long-nosed gar).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;		
OC	Lepisosteus.		
OX	NCBI_TaxID=34771;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Anemiyva Y., Youson J.H.;		
RX	PubMed=14697312;		
RT	"Primary structure of stanniocalcin in two basal Actinopterygii.";		
RL	Gen. Comp. Endocrinol. 135:250-257(2004).		
DR	EMBL; AB106623; BAC6164.1; -		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0005179; F:hormone activity; IEA.		
DR	InterPro; IPR000719; Prot Kinase.		
DR	InterPro; IPR004978; Stanniocalcin.		
DR	Pfam; PF03298; Stanniocalcin; 1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.		
KW	Signal.		
FT	SIGNAL	1	32
FT	CHAIN	33	252
FT	SEQUENCE	252 AA; 27936 MW; 2C99E88DDCED2E33 CRC64;	
Alignment Scores:			
Pred. No.:	4,24e-52	Length:	252
Score:	779.50	Matches:	152

Percent Similarity:	77.17%	Conservative:	44
Best Local Similarity:	59.84%	Mismatches:	9
Query Match:	11.41%	Indels:	9
DB:	2	Gaps:	3
US-09-703-350B-75 (1-3900) x Q80014 (1-252)			
QY	285	ATGCTCCAAACATCAGCAGACAGTGGTCTTGATGCTGGTGCATGCTGCTCTGCAACCCATGAG	3444
DB	1	MetLeuAaGlySerThyLLeuLeuLeuLeuLeuLeuLeuThrSerAla--TyrGln	19
QY	345	GCCGACCAATAGACTCTGTGAGCCGCCAGAAATCCGACGTGGCGGCTCAAACTCAGCT	404
DB	20	LeuAspGlnAsnGlnSerPheSerProArgThrArgValSerThrHisSerProSer	39
QY	405	GAAGTGGTTCGTGCTCAACAGTGTCTTACAGGTGGGCTGGGGCTTTTGATGCTGTG	464
DB	40	AspValAlaArgCysLeuAsnSerLLeuGlnValGlyCysGlyAlaPheAlaCysLeu	59
QY	465	GAATACTCAGCTGGAGACACATGGATGGATGATGATCATCTTAATCCTCTTGACAGC	524
DB	60	GlnAsnSerThrCysAspSphrSbpGlyMetHisAspLeuIleCysLysSerPheLeuTyrSer	79
QY	525	GCTGCTAAATTGACACTCAGGAAAGACATTGCTCAAGAGACCTTAAATGATGATGCC	584
DB	80	AlaAlaLysPheAspHrcGlnGlnGlySerValPheValLysGlnSerLeuLysCysIleAla	99
QY	585	AACGGGGTCACTCCCAAGGCTTCTGCTGCCAATTCGGAGGCTGCTCAGCTTCCAAAGGATG	644
DB	100	AsnGlyLysLeuSerLysValPheLeuThrLLeaArgArgCysSerThrPheGlnArgMet	119
QY	645	ATTGCTAGAGGTGACAGAAAGTGTCTACAGCAAGCTGATGTGTGCAGATCGCCACGCG	704
DB	120	IleSerGlnValGlnGlnGlnLysCysLysSerLysLeuAspLeuIleCysGlyValAlaLysLeu	139
QY	705	AACCTCGAAGCCATCACTGAGGTGCTCCAGCTGCCCAATCACTTCTCCACAGATACTAT	764
DB	140	AsnProAspAlaIleSerGlnValAlaGlnLeuProSerHisPheProAsnArgTyrTyr	159
QY	765	AACAGACTGTGTCGGAAGCTGTGTAAGTATGATGAAGACAGACAGACATCAGACAGAC	824
DB	160	SerLysLeuLeuGlnSerLeuMetLysAspSbpGlyMetLysLeuValArgSer	179
QY	825	AGCTGATGAGAAATTTGGGCTTAAATGSCCAGGCTTTTCCATCCTTCGACAGACAGAC	884
DB	180	SerLeuValSerArgLeuGlyProGlnMetLLeuPheGlnLeuLeuGlnSerLys	199
QY	885	CAGTGGCCCAACACACCCACGACGTGAC-----TTCAACAGG	923
DB	200	ProCysProSerSerSerSerSerLeuSerSerProAlaGlyAlaGlyArgGlyAsnTrp	219
QY	924	AGACGACCAATAGACCCGACAGAGCTGAAAGTCTCTCTCAGAAACCTCGAGGTAGAGAG	983
DB	220	ArgTrpProIleGlyProHisValAlaPheLys--MetGlnProLeuLeuArgArgGlnPro	238
QY	984	GACTCTCCTCCCAATCAAGACACATCCCATAGAGGTGA	1025
DB	239	SerThrLeuPheSerLysArgSerLLeaAspAspSerSer	252
RESULT 13			
STC ANGAU			
ID	STC ANGAU	STANDARD:	PRT: 250 AA.
AC	p18301.		
DT	01-NOV-1990 (rel. 16, Created)		
DT	15-JUN-1998 (rel. 36, Last sequence update)		
DT	05-JUN-2004 (rel. 44, Last annotation update)		
DE	Stannicalcain precursor (STC) (Corpuclules of Stannin protein) (CS)		
DE	(Hypocalcain) (Teleocalcain).		
GN	Name=STC:		
OS	Anguilla australis (Australian eel).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;		
OC	Anguilla.		



stimulates phosphate reabsorption by renal proximal tubules. The consequence of this action is increased levels of plasma phosphate, which combines with excess calcium and promotes its disposal into bone and scales.

-1- SUBUNIT: Homodimer; disulfide-linked.

-1- SUBCELLULAR LOCATION: Secreted.

-1- TISSUE SPECIFICITY: Produced and secreted by the corpuscles of Stannius.

-1- SIMILARITY: Belongs to the stannocalcin family.

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EMBL; S59519; AAB26419.1; -.

DR PIR; B60841; B60841.

DR PIR; I51197; I51197.

DR InterPro; IPR004978; Stannocalcin.

DR Pfam; PF03298; Stannocalcin.1.

KW Calcium transport; Direct protein sequencing; Glycoprotein; Hormone; Signal.

FT SIGNAL 1 18 Potential.

FT PROPEP 19 33 By similarity.

FT CHAIN 34 256 Stannocalcin.

FT CARBOHYD 62 62 N-linked (GlcNAc...).

SQ SEQUENCE 256 AA; 28074 MW; E68B8930B394A8D3 CRC64;

Alignment Scores:

Pred. No.:	6,28e-43	Length:	256
Score:	662.50	Matches:	125
Percent Similarity:	73.08%	Conservative:	46
Best Local Similarity:	53.42%	Mismatches:	54
Query Match:	9.70%	Indels:	9
DB:	1	Gaps:	4

US-09-703-350b-75 (1-3900) x STC\_ONCKI (1-256)

QY 315 CTGGTATAGAGTCTTCTGCAACCCATGAGCGGAGAGATGATCTCTGAGCCCGAG 374

DB 12 LeValValLeuGlyThyrAlaIathrPheAspThrAspProGluGluAa--SerProArg 30

QY 375 AAATCCGAGTGGCGGCTCAAAACTGACGCTGAAGTGGTTCGCTTCAACAGTCTCTA 434

DB 31 ArgAlaIarGpSerSerSerSerSerProSerAspValAlaIarGylLeuAsnGlyAlaLeu 50

QY 435 CAGGTGGCTGGCGGCGCTTTTGATGCTCGGAAACTCCACTGTGACACAGATGGAGTG 494

DB 51 AlavaGlyGylGlyThyrPheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMet 70

QY 495 TATGACATGTAATCTTCTTGTACAGCGCTGCTGAATTTGACACATCGAGGAAGAAGA 554

DB 71 HisAspGlyCysGlnLeuPhePheHisThrAlaAlaIathrPheAsnThrGlnGlyThr 90

QY 555 TTGCTGCAAGAGAGCTTAAATATGATCGCAACGGGGTCACTCCAAAGGCTCTTCTCGCC 614

DB 91 PheValValGluSerLeuArgCysIleAlaAsnGlyValThrSerValPheGlnThr 110

QY 615 ATTGGAGGTGCTCCACTTTCAGAAAGATGATGGCGAGGTCGAGGAAGAGTGTACAGC 674

DB 111 ILeArgArgCysGlyValPheGlnArgMetIleSerGluValGlnGluGlnCysTyrSer 130

QY 675 AAGCTGAATGTGTGACATCGCAACGCAACCCCTGAAGCCATCATGAGGTCTGCGAG 734

DB 131 ArgLeuAspGlyCysGlyValAlaIarGylSerAsnProGluAlaIleGlyGluValValGln 150

QY 735 CTGCGCAATCTTCTCCAAAGATCTATAACAGACTTGTCCGAAAGCTGTGGAAGGT 794

DB 151 ValProAlaHisPheProAsnArgIlyrThrSerThrLeuLeuGlnSerLeuValaCys 170

795 GATGAGACACAGTCCAGACATCAGAGACAGCTGATGAGAAATTTGGGCTTAACATG 854

DB 171 AspGluGlnThrValAlaValAlaArgAlaGlyLeuValAlaArgLeuGlyProAspMet 190

QY 855 GCCAGCCTCTTCCACATCTGTGACAGACAGACCTGTGCCCCAACAACCCACGAGCTGAC 914

DB 191 GluThrLeuPheGlnLeuLeuGlnAsnLysHisCysProGlnGlySerAsnGlnGlyPro 210

QY 915 TTCACAC-----AGAGACGCAACCATATAGCCCGCAAGACTGAAAGTCTCTC 959

DB 211 AsnSerAlaProAlaGlyThrPArgTrpPrometGlySerProSerPheValIle--- 229

QY 960 CTCGAAACCTCCGAGGTGAGAGACTCTCCCTCCACATC 1001

DB 230 GlnProSerMetArgGlyArgAsp-----ProThrHisLeu 241

RESULT 15

ID	STC_ONCKY	STANDARD;	PRT;	256 AA.
AC	P43648; Q98SEI;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Stannocalcin precursor (STC) (Corpuscles of Stannius protein) (CS)			
DE	(Hypocalcin) (Teleocalcin).			
GN	Name=STC;			
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;			
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.			
OX	NCBI_TaxID=8022;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Ovary;			
RA	McCluskey C.R.; Wagner G.F.;			
RT	"Rainbow trout ovarian stannocalcin";			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE OF 34-66.			
RC	TISSUE=Stannius corpuscles;			
RX	MEDLINE=88196801; PubMed=3360288;			
RA	Lafaber P.P.J.G.; Hansen R.G.J.M.; Choy Y.M.; Filk G.;			
RT	Herrmann-Erlee M.P.M.; Pang P.K.T.; Wendelaar Bonga S.E.;			
RT	"Identification of hypocalcin (teleocalcin) isolated from trout Stannius corpuscles.";			
RL	Gen. Comp. Endocrinol. 69:19-30(1988).			
CC	-1- FUNCTION: Its primary function is the prevention of hypercalcemia.			
CC	Upon release into the circulation, it lowers calcium transport by the gills, thereby reducing its rate of influx from the environment into the extracellular compartment. STC also stimulates phosphate reabsorption by renal proximal tubules. The consequence of this action is increased levels of plasma phosphate, which combines with excess calcium and promotes its disposal into bone and scales.			
CC	-1- SUBUNIT: Homodimer; disulfide-linked.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: Produced and secreted by the corpuscles of Stannius.			
CC	-1- SIMILARITY: Belongs to the stannocalcin family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	EMBL; AF36317; AK01423.1; -.			
DR	EMBL; AF36318; AK01424.1; -.			
DR	InterPro; IPR004978; Stannocalcin.			
DR	Pfam; PF03298; Stannocalcin.1.			
KW	Calcium transport; Direct protein sequencing; Glycoprotein; Hormone;			



